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PA 2002 00533 10 April 2002 (10.04.2002) DK
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- (72) Inventors; and
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- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.
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18 March 2004
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(54) Title: BACILLUS LICHENIFORMIS MUTANT HOST CELL

(57) Abstract: A *Bacillus licheniformis* mutant host cell comprising a mutation (deletion) in one or more genes encoding polypeptides involved in sporulation wherein the mutant host cell expresses at least 5% less of the one or more polypeptides involved in sporulation than the parent host cell, when cultivated under comparable conditions. The mutant host cell is used for producing heterologous polypeptides.



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INTERNATIONAL SEARCH REPORT

International Application No

PCT/DK 03/00200

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/75 C12N1/21 C07K14/32

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 97 03185 A (NOVONORDISK AS ;PRIEST FERGUS G (GB); FLEMING ALASTAIR B (GB); TAN) 30 January 1997 (1997-01-30) the whole document	1-21
X	--- FLEMING A B ET AL: "Extracellular enzyme synthesis in a sporulation-deficient strain of Bacillus licheniformis." APPLIED AND ENVIRONMENTAL MICROBIOLOGY, vol. 61, no. 11, November 1995 (1995-11), pages 3775-3780, XP002902964 ISSN: 0099-2240 abstract	1-21
X	--- WO 98 22598 A (NOVO NORDISK BIOTECH INC) 28 May 1998 (1998-05-28) page 6, line 8 - line 11; claims 1,2,17 --- -/-	1-21

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

15 July 2003

Date of mailing of the international search report

28. 10. 2003

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Ida Christensen

INTERNATIONAL SEARCH REPORT

Interr Application No

PCT/DK 03/00200

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>WO 02 00907 A (JOERGENSEN STEEN TROELS ;OLSEN CARSTEN (DK); NOVOZYMES AS (DK); AN) 3 January 2002 (2002-01-03) claims -----</p>	6,7

INTERNATIONAL SEARCH REPORT

International application No.
PCT/DK 03/00200

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-21 (partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1 : claims 1-21 (partially).

A *Bacillus licheniformis* mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: 2.

Invention 2 : claims 1-21 (partially).

A *Bacillus licheniformis* mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: 4.

Invention 3: claims 1-21 (partially).

A *Bacillus licheniformis* mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: 6

Invention 4 : claims 1-21 (partially).

A *Bacillus licheniformis* mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No:

etc....

etc....

etc....

Invention 96 :claims 1-21 (partially).

A *Bacillus licheniformis* mutant host cell, which is mutated in at least one gene encoding a polypeptide involved in sporulation, which polypeptide is at least 80% identical to the polypeptide shown in SEQ ID No: 191.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/DK 03/00200

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9703185	A	30-01-1997	AU 6353896 A CN 1190434 A WO 9703185 A1 EP 0837925 A1 JP 11509096 T	10-02-1997 12-08-1998 30-01-1997 29-04-1998 17-08-1999
WO 9822598	A	28-05-1998	AT 246251 T AU 5445098 A DE 69723855 D1 EP 0941349 A1 JP 2001503641 T WO 9822598 A1 US 5958728 A	15-08-2003 10-06-1998 04-09-2003 15-09-1999 21-03-2001 28-05-1998 28-09-1999
WO 0200907	A	03-01-2002	AU 6583501 A CN 1437656 T WO 0200907 A1 EP 1297170 A1 US 2003032186 A1	08-01-2002 20-08-2003 03-01-2002 02-04-2003 13-02-2003

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SEQUENCE LISTING

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Andersen, Jens Tønne
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 tgattgtaat ggtacatgta tacactgttt atcatagttt aataatgaat atgatcaatg 480
 aatgaaagga gagcttagtc atg ttt cat tgc aaa cca aat gtg atg ccg cca 533
 Met Phe His Cys Lys Pro Asn Val Met Pro Pro
 1 5 10

10295.204.ST25.txt

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Ile Val His Pro Thr Asn Cys Cys Gln Thr His Thr Phe Ser Lys Thr
15 20 25

att gtg ccg cat att cat ccg cag cat ata aca aat gtg cat cat aag      629
Ile Val Pro His Ile His Pro Gln His Ile Thr Asn Val His His Lys
30 35 40

cat ttc cag cat gtg cat caa tat cca cac act tat tct agt tac gat      677
His Phe Gln His Val His Gln Tyr Pro His Thr Tyr Ser Ser Tyr Asp
45 50 55

cct gtt aca cac tct cat act cat tgt ggt aaa cca tgt tgt aac      722
Pro Val Thr His Ser His Thr His Cys Gly Lys Pro Cys Cys Asn
60 65 70

tagtgggatt aaacaatgac tgtatggttt acagtgcatt atcatatata gcacc'aact      782
gggtgctttt ttatgttctc tgtaaaccgg gtccagtaaa tctcagaata aacgattggc      842
ggccaatgag agcctctgag tgtggggcccg gtttagaaag aatataccag gcgctttccc      902
aaacgagagg gcgtttttta tttagaggag atgatccaaa tggaatcgaa atgcaagcat      962
tgcggtgagg ttcatggagt ttatttgcga gaggagaaaa gggagaatgg cgttgaaatt      1022
gggtatatcc aatgccccgc ctgccagcat agggccgtgt tttctgtgac tacc'ccacaa      1082
attagagtcc tccaaaagcg tattagaggt gtaaagaacc aatatgcgaa agccaagagg      1142
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His Pro Gln His Ile Thr Asn Val His His Lys His Phe Gln His Val
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His Thr His Cys Gly Lys Pro Cys Cys Asn
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10295.204.ST25.txt

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<222> (501)..(1046)

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aacgaccttc ttcagcttgt cgcgcataca atatcaaacc aagtgacaaa cgagatcatc      180
acatcgaccg ggggagacct gctgaaaggc gagaccgggtt caaaagtgaa aaattcatca      240
ccgagctggt ctctataatt tggcggcgcc ttttaaggcg ccgttttttt tgaattcaat      300
ttcccgccgc gacggcttat tgaaaagatt cgtttttcgg ctgtcttttt cttttctgat      360
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aaacaaggag gcatgaccga atg tct gaa tac agg gaa att atc act aaa gcg      533
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gtg gtc gcg aaa ggc cgg aaa ttc acc cag tcc act cat aca atc tcc      581
Val Val Ala Lys Gly Arg Lys Phe Thr Gln Ser Thr His Thr Ile Ser
                    15             20             25

cct tcg caa aag cca acc agt att tta ggc ggt tgg att atc aat cat      629
Pro Ser Gln Lys Pro Thr Ser Ile Leu Gly Gly Trp Ile Ile Asn His
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aag tat gac gct gaa aaa atc gga aaa acc gtg gaa att gaa ggg aca      677
Lys Tyr Asp Ala Glu Lys Ile Gly Lys Thr Val Glu Ile Glu Gly Thr
                    45             50             55

tat gat atc aac gtc tgg tat tca tat gcg gac aac acc aaa acc gaa      725
Tyr Asp Ile Asn Val Trp Tyr Ser Tyr Ala Asp Asn Thr Lys Thr Glu
60             65             70             75

gtt gtg aca gaa cgc gtt tcc tat gtt gat gtc att aag ctc cgg tat      773
Val Val Thr Glu Arg Val Ser Tyr Val Asp Val Ile Lys Leu Arg Tyr
80             85             90

cgc gac aaa aat tac tta gat gat gaa cac gaa gtc att gcg aaa gtg      821
Arg Asp Lys Asn Tyr Leu Asp Asp Glu His Glu Val Ile Ala Lys Val
95             100             105

ctt cag cag ccg aac tgc ctt gaa gtg acc att tct ccg aac gga aac      869
Leu Gln Gln Pro Asn Cys Leu Glu Val Thr Ile Ser Pro Asn Gly Asn
110             115             120

aaa gtg gtt gta cag gcg gaa aga gaa ttt tta gca gag gtc gtc ggc      917
Lys Val Val Val Gln Ala Glu Arg Glu Phe Leu Ala Glu Val Val Gly
125             130             135

gag acg aag gtc gtc gtt gag gtc aat tct gat tgg acg gaa agc gat      965
Glu Thr Lys Val Val Val Glu Val Asn Ser Asp Trp Thr Glu Ser Asp
140             145             150             155

gaa gaa gaa gcg tgg gaa gaa gag ctt gat gaa gaa ctt gag gat atc      1013
Glu Glu Glu Ala Trp Glu Glu Glu Leu Asp Glu Glu Leu Glu Asp Ile
160             165             170

aat ccc gag ttt ttg gtt gga gat cca gaa gaa taaaaggaag ctagggaaac      1066
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10295.204.ST25.txt
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caatatttaa agattaaggc agagtatcag gatgcctttt ttttttttcg tcttggcgac 1246
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gtc 1549

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Thr Ser Ile Leu Gly Gly Trp Ile Ile Asn His Lys Tyr Asp Ala Glu
35 40 45

Lys Ile Gly Lys Thr Val Glu Ile Glu Gly Thr Tyr Asp Ile Asn Val
50 55 60

Trp Tyr Ser Tyr Ala Asp Asn Thr Lys Thr Glu Val Val Thr Glu Arg
65 70 75 80

Val Ser Tyr Val Asp Val Ile Lys Leu Arg Tyr Arg Asp Lys Asn Tyr
85 90 95

Leu Asp Asp Glu His Glu Val Ile Ala Lys Val Leu Gln Gln Pro Asn
100 105 110

Cys Leu Glu Val Thr Ile Ser Pro Asn Gly Asn Lys Val Val Val Gln
115 120 125

Ala Glu Arg Glu Phe Leu Ala Glu Val Val Gly Glu Thr Lys Val Val
130 135 140

Val Glu Val Asn Ser Asp Trp Thr Glu Ser Asp Glu Glu Glu Ala Trp
145 150 155 160

10295.204.ST25.txt

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Val Gly Asp Pro Glu Glu
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 gaatgttcca tgtgaaacag tgtcagtcga gaaaccccgga tttttcttta tttttctttc 240
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 Met Thr Thr Lys Thr Leu Ala Trp His Glu Thr
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 15 20 25
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 Ile Lys Lys Ser Met Lys Lys Ile Ser Asp Pro Gln Leu Arg Gln Leu
 30 35 40
 tac agc gtg tca gca aaa gca ttg gag caa aat tta aga gag ctt ctt 677
 Tyr Ser Val Ser Ala Lys Ala Leu Glu Gln Asn Leu Arg Glu Leu Leu
 45 50 55
 ccc ttt ttg cca aaa gct cca gca ttt cag cgg gag gat gaa cgg gct 725
 Pro Phe Leu Pro Lys Ala Pro Ala Phe Gln Arg Glu Asp Glu Arg Ala
 60 65 70 75
 gac ttg tat ttt gat gcg ggt gat ctg ttg gtg ctg gcg aaa acg acc 773
 Asp Leu Tyr Phe Asp Ala Gly Asp Leu Leu Val Leu Ala Lys Thr Thr
 80 85 90
 gtt cga aac tat gcg att gcg atc acg gaa acg gcg acg ccc gag ctc 821
 Val Arg Asn Tyr Ala Ile Ala Ile Thr Glu Thr Ala Thr Pro Glu Leu
 95 100 105
 agg aga gtg ctt gtt aaa caa atc aat gcg gcc att aag ttg cat gaa 869
 Arg Arg Val Leu Val Lys Gln Ile Asn Ala Ala Ile Lys Leu His Glu
 110 115 120
 caa gtt ttt tat ttt atg tac caa aga ggc tta tat ccc gcc tat aac 917

10295.204.ST25.txt

Gln Val Phe Tyr Phe Met Tyr Gln Arg Gly Leu Tyr Pro Ala Tyr Asn
 125 130 135
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 140 145 150
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 Ser Met Arg
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 20 25 30

Lys Lys Ile Ser Asp Pro Gln Leu Arg Gln Leu Tyr Ser Val Ser Ala
 35 40 45

Lys Ala Leu Glu Gln Asn Leu Arg Glu Leu Leu Pro Phe Leu Pro Lys
 50 55 60

Ala Pro Ala Phe Gln Arg Glu Asp Glu Arg Ala Asp Leu Tyr Phe Asp
 65 70 75 80

Ala Gly Asp Leu Leu Val Leu Ala Lys Thr Thr Val Arg Asn Tyr Ala
 85 90 95

Ile Ala Ile Thr Glu Thr Ala Thr Pro Glu Leu Arg Arg Val Leu Val
 100 105 110

Lys Gln Ile Asn Ala Ala Ile Lys Leu His Glu Gln Val Phe Tyr Phe
 115 120 125

Met Tyr Gln Arg Gly Leu Tyr Pro Ala Tyr Asn Leu Val Asp Leu Leu
 Page 12

10295.204.ST25.txt
140

130

135

Lys Gly Asp Ala Met His Ala Gln Lys Ala Ile Ser Met Arg
145 150 155

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<212> DNA
<213> Bacillus licheniformis

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cggctctgctt ccgggacagg tttttttcac atatgatatg tcagctgaaa aaggaggaaa 180
tg atg atg agt gcc act gcc ttg ccg gcc ttt agg ctg cac att cat 227
Met Met Ser Ala Thr Ala Leu Pro Ala Phe Arg Leu His Ile His 15
1 5 10
ccg aag cat ctg ctt gag ttg aaa aaa gac gtc tgg agt gat gaa gcc 275
Pro Lys His Leu Leu Glu Leu Lys Lys Asp Val Trp Ser Asp Glu Ala 30
20
gtt ccc ggc atg ctc ttg acc ggt tca gca aag acg cct gtc gca gtg 323
Val Pro Gly Met Leu Leu Thr Gly Ser Ala Lys Thr Pro Val Ala Val 45
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tca tac aga ggg gcc cac acc cgc aaa ctg acg aaa aaa tcc tat ttc 371
Ser Tyr Arg Gly Ala His Thr Arg Lys Leu Thr Lys Lys Ser Tyr Phe 60
50
att caa tat ccg gac aat aaa gaa aag gct gcg ttt cat ttg aac gcg 419
Ile Gln Tyr Pro Asp Asn Lys Glu Lys Ala Ala Phe His Leu Asn Ala 75
65 70
gaa tat cat gat ccg tct ttc atc aga aac agg ctt tcc ttt cat ttt 467
Glu Tyr His Asp Pro Ser Phe Ile Arg Asn Arg Leu Ser Phe His Phe 90
80 85
ttt gaa caa atc ggc gtc ctt gcg cca gca gca tca cac gtt ttc ctt 515
Phe Glu Gln Ile Gly Val Leu Ala Pro Ala Ala Ser His Val Phe Leu 100
105 110
tat atc aat gaa aaa aaa gaa ggc atc tat tta aaa atc gaa tct gtt 563
Tyr Ile Asn Glu Lys Lys Glu Gly Ile Tyr Leu Lys Ile Glu Ser Val 115
120
gac gat cat ttc tta aag agg aga aat tta gaa agg ggg gcc att tat 611
Asp Asp His Phe Leu Lys Arg Arg Asn Leu Glu Arg Gly Ala Ile Tyr 130
135 140
tat gcc gtt gat gac gat gct aat ttt tct ctg ctg agt tcc ttc aat 659
Tyr Ala Val Asp Asp Ala Asn Phe Ser Leu Leu Ser Ser Phe Asn 145
150 155
aaa aag gct aag caa aat ctc atg cag gga tac gaa aga aaa acg ggt 707
Lys Lys Ala Lys Gln Asn Leu Met Gln Gly Tyr Glu Arg Lys Thr Gly 160
165 170 175

10295.204.ST25.txt

tca agc cgc cac gat gac tac ctc cat gag ttt atc tac ttt atc aat 755
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 180 185 190
 acc gcc aaa gac gac ata ttt gaa aaa gaa atc aaa cgc tat ctc gat 803
 Thr Ala Lys Asp Asp Ile Phe Glu Lys Glu Ile Lys Arg Tyr Leu Asp
 195 200 205
 gtc aaa caa tat ttg ctg tgg ctc atc ggc gcc gtc tgc acc caa aat 851
 Val Lys Gln Tyr Leu Leu Trp Leu Ile Gly Ala Val Cys Thr Gln Asn
 210 215 220
 ttc gac ggc ttt gtc cat aat tac gcg ctt tat tta aac ggt cgc aca 899
 Phe Asp Gly Phe Val His Asn Tyr Ala Leu Tyr Leu Asn Gly Arg Thr
 225 230 235
 aaa acg ttt caa atc att cca tgg gat tat gac gcg aca tgg gga cgg 947
 Lys Thr Phe Gln Ile Ile Pro Trp Asp Tyr Asp Ala Thr Trp Gly Arg
 240 245 250 255
 aat att cac ggg gaa gaa atg gag cac aac cgg att ccg gcg aaa ggc 995
 Asn Ile His Gly Glu Glu Met Glu His Asn Arg Ile Pro Ala Lys Gly
 260 265 270
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 Tyr Asn Thr Leu Ser Ala Arg Leu Leu Asp Ile Pro Ala Phe Gln Ser
 275 280 285
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 Gln Tyr Phe Asn Leu Met Lys Asn Val Leu His Arg Gln Phe Thr Ile
 290 295 300
 agc cgg ctt tcg cgg tat gcg gta aac tgg cac gag aca atc gcg cct 1139
 Ser Arg Leu Ser Arg Tyr Ala Val Asn Trp His Glu Thr Ile Ala Pro
 305 310 315
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 Phe Leu Glu His Asp Pro Tyr Thr Thr Val Thr Tyr Ser Arg Leu Glu
 320 325 330 335
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 340 345 350
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10295.204.ST25.txt

<213> Bacillus licheniformis

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 20 25 30

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 35 40 45

Tyr Arg Gly Ala His Thr Arg Lys Leu Thr Lys Lys Ser Tyr Phe Ile
 50 55 60

Gln Tyr Pro Asp Asn Lys Glu Lys Ala Ala Phe His Leu Asn Ala Glu
 65 70 75 80

Tyr His Asp Pro Ser Phe Ile Arg Asn Arg Leu Ser Phe His Phe Phe
 85 90 95

Glu Gln Ile Gly Val Leu Ala Pro Ala Ala Ser His Val Phe Leu Tyr
 100 105 110

Ile Asn Glu Lys Lys Glu Gly Ile Tyr Leu Lys Ile Glu Ser Val Asp
 115 120 125

Asp His Phe Leu Lys Arg Arg Asn Leu Glu Arg Gly Ala Ile Tyr Tyr
 130 135 140

Ala Val Asp Asp Asp Ala Asn Phe Ser Leu Leu Ser Ser Phe Asn Lys
 145 150 155 160

Lys Ala Lys Gln Asn Leu Met Gln Gly Tyr Glu Arg Lys Thr Gly Ser
 165 170 175

Ser Arg His Asp Asp Tyr Leu His Glu Phe Ile Tyr Phe Ile Asn Thr
 180 185 190

Ala Lys Asp Asp Ile Phe Glu Lys Glu Ile Lys Arg Tyr Leu Asp Val
 195 200 205

Lys Gln Tyr Leu Leu Trp Leu Ile Gly Ala Val Cys Thr Gln Asn Phe
 210 215 220

Asp Gly Phe Val His Asn Tyr Ala Leu Tyr Leu Asn Gly Arg Thr Lys
 225 230 235 240

Thr Phe Gln Ile Ile Pro Trp Asp Tyr Asp Ala Thr Trp Gly Arg Asn
 245 250 255

Ile His Gly Glu Glu Met Glu His Asn Arg Ile Pro Ala Lys Gly Tyr
260 265 270

Asn Thr Leu Ser Ala Arg Leu Leu Asp Ile Pro Ala Phe Gln Ser Gln
275 280 285

Tyr Phe Asn Leu Met Lys Asn Val Leu His Arg Gln Phe Thr Ile Ser
290 295 300

Arg Leu Ser Arg Tyr Ala Val Asn Trp His Glu Thr Ile Ala Pro Phe
305 310 315 320

Leu Glu His Asp Pro Tyr Thr Thr Val Thr Tyr Ser Arg Leu Glu Asp
325 330 335

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340 345 350

Leu Phe Glu Leu Ser Arg
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cggatcagac ggaatcctat tggagctgga aaagaagtcc ttggccatgg caagtttaat 480
agaggaaggg agtcagggttc atg tgg ctt tat gag aaa aaa ctg cag tat cct 533
Met Trp Leu Tyr Glu Lys Lys Leu Gln Tyr Pro
1 5 10

gtt agg gtg aga gaa tgc aat ccg aga ctt gcc aaa ttt ttg att gag 581
Val Arg Val Arg Glu Cys Asn Pro Arg Leu Ala Lys Phe Leu Ile Glu
15 20 25

caa tac ggc gga gcg gac ggc gaa ttg gct gcg gcg ctt cgc tat ttg 629
Gln Tyr Gly Gly Ala Asp Gly Glu Leu Ala Ala Ala Leu Arg Tyr Leu
30 35 40

aac cag cgc tac agc ata ccc gat aaa gtc gtc gga ctg ctg acg gac 677
Page 16

10295.204.ST25.txt

Asn Gln Arg Tyr Ser Ile Pro Asp Lys Val Val Gly Leu Leu Thr Asp
 45 50 55
 atc ggt acg gaa gag ttt gct cac ctt gaa atg att gcc acg atg gta 725
 Ile Gly Thr Glu Glu Phe Ala His Leu Glu Met Ile Ala Thr Met Val 75
 60
 tat aaa tta aca aaa gac gcg acg ccc gag cag atg aag gaa gcc ggg 773
 Tyr Lys Leu Thr Lys Asp Ala Thr Pro Glu Gln Met Lys Glu Ala Gly 90
 80
 ctc ggc gat cat tac gca gac cat gac aaa gcc ctg ttt tat cat aac 821
 Leu Gly Asp His Tyr Ala Asp His Asp Lys Ala Leu Phe Tyr His Asn 105
 95
 gct gcc ggc gtt ccg ttc acc gct aca tac atc cag gca aaa ggc gat 869
 Ala Ala Gly Val Pro Phe Thr Ala Thr Tyr Ile Gln Ala Lys Gly Asp 120
 110
 ccg att gcc gat tta tat gaa gat ata gcg gct gaa gaa aaa gcg agg 917
 Pro Ile Ala Asp Leu Tyr Glu Asp Ile Ala Ala Glu Glu Lys Ala Arg 135
 125
 gct acg tat caa tgg ctg att gac atg tcg gat gat ccg gat tta aat 965
 Ala Thr Tyr Gln Trp Leu Ile Asp Met Ser Asp Asp Pro Asp Leu Asn 155
 140
 gac ggc ctg gcg ttt tta cgg gaa agg gaa atc gtt cat tca cag cgc 1013
 Asp Gly Leu Ala Phe Leu Arg Glu Arg Glu Ile Val His Ser Gln Arg 170
 160
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 Phe Arg Glu Ala Val Glu Ile Leu Lys Glu Glu Arg Asp Arg Lys Lys 185
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 Val Phe
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 Page 17

10295.204.ST25.txt
25

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Asp Ala Thr Pro Glu Gln Met Lys Glu Ala Gly Leu Gly Asp His Tyr
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Tyr Glu Asp Ile Ala Ala Glu Glu Lys Ala Arg Ala Thr Tyr Gln Trp
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Ser	Trp	Ile	Ala	Leu	Asp	Pro	Glu	Cys	Glu	His	Pro	Gly	Asn	Asp	Tyr			
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Cys	Gly	Arg	Lys	Gly	Gln	Asn	Gly	Phe	Ile	Asp	Ser	Asp	Leu	Asp	Gln			
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 50 55 60

Thr Ile Ile Ile Lys Asp Ser Cys Asp Val Gln Val Ser Thr Glu Asp
 65 70 75 80

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 85 90 95

Thr Ile Ile Leu Ala Ile Ile Asp Asp Pro Asp Leu Ala Glu Leu Val
 100 105 110

Thr Thr Asp Leu Leu Gln Val Thr Ala Asn Lys Gln Thr Asn Arg Gln
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Lys Leu Val Ile Asp Asn Ser Arg Asn Val His Val Thr Thr Glu Asp
 130 135 140

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10295.204.ST25.txt

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 15 20 25

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 Ala Thr Asn Val Asn Asn Arg Ala Gly Asn Gly Asn Pro Val Pro Thr
 30 35 40

ggc gat gga act tac agc cgg gga gac atg aat tat cac aac cat ttg 677
 Gly Asp Gly Thr Tyr Ser Arg Gly Asp Met Asn Tyr His Asn His Leu
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 Val Asn Thr Ala Asp Thr Gly Tyr Asp Arg Pro Glu Asn Arg Lys Ile
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tca agg aat atc act ggg cgc gtc aac aaa ttg aat tat gtt gac gaa 773
 Ser Arg Asn Ile Thr Gly Arg Val Asn Lys Leu Asn Tyr Val Asp Glu
 80 85 90

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 95 100 105

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 110 115 120

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 Lys Thr Phe Ala Gly Asp Arg Thr Val Gln Val Val Glu Asp Asp Gly
 125 130 135

gca ttt aca agg ctg cgc gaa atg aac gat gat cct cag aac att agg 965
 Ala Phe Thr Arg Leu Arg Glu Met Asn Asp Asp Pro Gln Asn Ile Arg
 140 145 150 155

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 Ser Arg Gly Asp Met Asn Tyr His Asn His Leu Val Asn Thr Ala Asp
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 Thr Gly Tyr Asp Arg Pro Glu Asn Arg Lys Ile Ser Arg Asn Ile Thr
 65 70 75 80
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 Thr Asn Glu Thr Val Ile Ile Ala Val Arg Ser Asp Lys Arg Leu Thr
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 Asn Asn Glu Arg Thr Gln Ile Arg Lys Ala Ala Lys Thr Phe Ala Gly
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10295.204.ST25.txt

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 Val Lys Glu Leu Thr Ala Thr Gly Arg Thr Val
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 Asp Glu Ala Val Gln Ser Gly Leu Glu Gln Leu Gly Leu His Ala Asp
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 Asp Val Glu Val Asp Val Val Asp Glu Gly Lys Lys Gly Leu Phe Gly
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 Pro Val Lys Glu Ala Lys Gln Tyr Leu Glu Asn Val Ile Ser Asn Met
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 80 85 90
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 Phe Gln Leu Lys Gly Asp Lys Thr Ala Leu Leu Ile Gly Lys Arg Gly
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 caa act tta aat gcc ctt gaa acg ctg acg cag ctc gtg ctc aat cgt 869
 Gln Thr Leu Asn Ala Leu Glu Thr Leu Thr Gln Leu Val Leu Asn Arg
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 cat tcc gac aga tat atc caa gcg gtg gtt gac gcc gaa gga tac cgc 917

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 cag gcg gcc agg cag aaa aaa gac att cac ctg gag ccg atg cct tcc
 Gln Ala Ala Arg Gln Lys Lys Asp Ile His Leu Glu Pro Met Pro Ser
 160 165 170 1013
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 Ser Glu Arg Lys Val Ile His Asp Thr Leu Ala Gly Tyr Ser Gln His
 175 180 185 1061
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 Ile Glu Thr Tyr Ser Thr Gly Glu Asp His Asn Arg His Leu Val Ile
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 35 40 45

Ser Ala Val Val Asn Ile Arg Glu Lys Ile Asp Pro Val Lys Glu Ala
 50 55 60

Lys Gln Tyr Leu Glu Asn Val Ile Ser Asn Met Gly Ile Gln Ala Gln
 65 70 75 80

Val Thr Ala Glu Glu Glu Ser Lys Arg Val Val Phe Gln Leu Lys Gly
 Page 25

10295.204.ST25.txt

85

90

95

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 100 105 110

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 115 120 125

Ile Gln Ala Val Val Asp Ala Glu Gly Tyr Arg Ala Lys Arg Lys Glu
 130 135 140

Thr Leu Ala Gln Leu Ala Leu Lys Leu Ala Asp Gln Ala Ala Arg Gln
 145 150 155 160

Lys Lys Asp Ile His Leu Glu Pro Met Pro Ser Ser Glu Arg Lys Val
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gac cga aac agc gtc atc att aca tgg gga aac atg gat atg aaa gtg Asp Arg Asn Ser Val Ile Ile Thr Trp Gly Asn Met Asp Met Lys Val 95 100 105			821
ctg aag caa aat tgc atg ttc aac cat gtt ccg ttt ccg ttt aaa gga Leu Lys Gln Asn Cys Met Phe Asn His Val Pro Phe Pro Phe Lys Gly 110 115 120			869
gag atg agg gac ctt tcc atg gag tac aag gaa ttt ttc ggc gac aaa Glu Met Arg Asp Leu Ser Met Glu Tyr Lys Glu Phe Phe Gly Asp Lys 125 130 135			917
aca ttg acg aat ttg tgg aag gca gcg gaa gag tac ggc gat tca gga Thr Leu Thr Asn Leu Trp Lys Ala Ala Glu Glu Tyr Gly Asp Ser Gly 140 145 150 155			965
acg gga aaa cag cat aaa gcg ctt gac gac gcg atg aca acg tat aag Thr Gly Lys Gln His Lys Ala Leu Asp Asp Ala Met Thr Thr Tyr Lys 160 165 170			1013
ttg ttt cgg ctc gta gaa cgg gat aag aag tat ttg gaa aat ccg aag Leu Phe Arg Leu Val Glu Arg Asp Lys Lys Tyr Leu Glu Asn Pro Lys 175 180 185			1061
ccg acg acg atc ggc gaa cgg gtt gac ctc tca aaa gtc ttt ccg cac Pro Thr Thr Ile Gly Glu Arg Val Asp Leu Ser Lys Val Phe Pro His 190 195 200			1109
gcc aca taaaaaaccc aatctgacaa acagattggg ttatttgtgc aggaaatatt Ala Thr 205			1165
ctttttcaag cccatgaata agctcaagcg attttgccgc gtattcggac gaatcgtttt			1225
gcagatccgt ttttaagcgg ctcaaagctg agcggagcga atccgcataa tccggtacag			1285
cttcacgaa cggcttcacc atgcggtgcg ggatattcgt ctgttcaccg taagcgagcg			1345
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<210> 24
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 <213> Bacillus licheniformis

10295.204.ST25.txt

<400> 24

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 20 25 30

Gly Ile Val Lys Thr Val His Asp Glu Val Val Glu Thr Phe Ser Ser
 35 40 45

Tyr Ile Lys Pro Lys Lys Phe Pro Lys Leu Thr Arg Arg Cys Lys Asn
 50 55 60

Phe Leu Ser Ile Thr Gln Glu Gln Val Asp Gln Gly Ile Thr Phe Asn
 65 70 75 80

Ala Leu Ile Glu Lys Leu Arg Glu Leu Asp Pro Asp Arg Asn Ser Val
 85 90 95

Ile Ile Thr Trp Gly Asn Met Asp Met Lys Val Leu Lys Gln Asn Cys
 100 105 110

Met Phe Asn His Val Pro Phe Pro Phe Lys Gly Glu Met Arg Asp Leu
 115 120 125

Ser Met Glu Tyr Lys Glu Phe Phe Gly Asp Lys Thr Leu Thr Asn Leu
 130 135 140

Trp Lys Ala Ala Glu Glu Tyr Gly Asp Ser Gly Thr Gly Lys Gln His
 145 150 155 160

Lys Ala Leu Asp Asp Ala Met Thr Thr Tyr Lys Leu Phe Arg Leu Val
 165 170 175

Glu Arg Asp Lys Lys Tyr Leu Glu Asn Pro Lys Pro Thr Thr Ile Gly
 180 185 190

Glu Arg Val Asp Leu Ser Lys Val Phe Pro His Ala Thr
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<210> 25

<211> 1600

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501)..(1097)

<400> 25

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ttccaaaatt	cagctccttt	tttggaggtc	attgtttttt	caacggtttc	tttgacagtt	180										
ttttcatcca	ttacaagtgt	ttcatttaaat	ttgtcatcat	ttaatatattc	ttgaatcgct	240										
ttttttccgt	catctgtctt	taatatatcg	acaaccattt	ttttggtttg	atcatagtc	300										
atctcagctg	cttggtccgt	gggagcacaa	gctgttacag	atagaaacag	aaaacagctt	360										
atcgatagca	ttgcggtctt	gaacatgctt	aagctctctt	cgaaaactcg	tcttaccttt	420										
aatatgaatg	tcttttaaaa	atttatacat	aacaaaatat	cgctgttaca	gcggtttatt	480										
tagggggttg	gaagtctaca	atg	aaa	agc	cgt	aat	ctc	gtc	cga	ttt	ttc	ttt	533			
		Met	Lys	Ser	Arg	Asn	Leu	Val	Arg	Phe	Phe	Phe				
		1				5					10					
tcc	gta	ttg	ggt	gtc	gga	gct	ttg	act	aca	agt	att	gtc	ggt	ttt	gcc	581
Ser	Val	Leu	Gly	Val	Gly	Ala	Leu	Thr	Thr	Ser	Ile	Val	Gly	Phe	Ala	
			15					20					25			
ata	gag	tgg	gga	aga	tat	aag	gag	ctg	ttt	ctt	tcc	ttc	gag	gta	ttg	629
Ile	Glu	Trp	Gly	Arg	Tyr	Lys	Glu	Leu	Phe	Leu	Ser	Phe	Glu	Val	Leu	
		30					35					40				
gag	att	ctg	tct	gtt	ctt	ttc	tgg	ttt	atc	ggg	gtt	ggc	atg	atc	ttt	677
Glu	Ile	Leu	Ser	Val	Leu	Phe	Trp	Phe	Ile	Gly	Val	Gly	Met	Ile	Phe	
	45					50					55					
agc	gtg	att	gct	caa	atg	gga	ttt	gtg	att	ttc	tta	acg	att	cac	cgc	725
Ser	Val	Ile	Ala	Gln	Met	Gly	Phe	Val	Ile	Phe	Leu	Thr	Ile	His	Arg	
					65					70					75	
ttt	gca	ctg	gaa	att	ttc	aga	tct	cat	tct	ttg	tgg	aat	tcg	att	cag	773
Phe	Ala	Leu	Glu	Ile	Phe	Arg	Ser	His	Ser	Leu	Trp	Asn	Ser	Ile	Gln	
				80					85					90		
ctg	ttt	ttg	att	ata	ttt	gtc	gcg	ttt	gac	ttg	gtt	tac	ttg	cgc	ttt	821
Leu	Phe	Leu	Ile	Ile	Phe	Val	Ala	Phe	Asp	Leu	Val	Tyr	Leu	Arg	Phe	
			95					100					105			
ctg	ttt	ttt	gaa	aaa	gat	gga	ggc	tcc	atc	att	ccg	tac	att	tgg	ctg	869
Leu	Phe	Phe	Glu	Lys	Asp	Gly	Gly	Ser	Ile	Ile	Pro	Tyr	Ile	Trp	Leu	
		110					115					120				
ccg	ctc	ttt	att	ttg	gcg	gta	ggc	att	gcg	gcc	gct	tat	gca	aag	caa	917
Pro	Leu	Phe	Ile	Leu	Ala	Val	Gly	Ile	Ala	Ala	Ala	Tyr	Ala	Lys	Gln	
						130					135					
aaa	cag	tcc	tct	aaa	aaa	acg	ttc	gtt	tcc	gca	tta	ttt	cta	atg	ttt	965
Lys	Gln	Ser	Ser	Lys	Lys	Thr	Phe	Val	Ser	Ala	Leu	Phe	Leu	Met	Phe	
					145					150					155	
gtt	ttt	act	gtg	atg	gag	tgg	ttc	ccg	gcg	tta	agg	gtc	aat	gaa	gag	1013
Val	Phe	Thr	Val	Met	Glu	Trp	Phe	Pro	Ala	Leu	Arg	Val	Asn	Glu	Glu	
				160					165					170		
gac	tgg	ctc	tat	tta	atg	ctg	ctt	cct	tta	tta	gcc	tgc	aac	gct	ttt	1061
Asp	Trp	Leu	Tyr	Leu	Met	Leu	Leu	Pro	Leu	Leu	Ala	Cys	Asn	Ala	Phe	
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10295.204.ST25.txt

tggcggaatc tgaagcgtga aagagcacga tgtcaccggc gtttaccggt ccatttacgt 1287
 tttggacgat cttttgaacc cccgggttcg tccagtcacg cgagttaata ctataatgaa 1347
 caacggtgta gccgtactgt ttagcaacat cgagtacgctc tttattaaac tggccggtcg 1407
 gcggtcttaa aagcgtaagg tcgtcaagcc cgagtttttg aaaggagtgt cgtgcttttg 1467
 ctaagtcttt tttgatctcg cttttcttca tttgcgaata gtttttataa gcatagccca 1527
 tactcccgat ctggtgacca tctttacgga ttctttctac gacatccggg tggcgctctg 1587
 cccatgaagc tga 1600

<210> 26
 <211> 199
 <212> PRT
 <213> Bacillus licheniformis

<400> 26

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Gly Ala Leu Thr Thr Ser Ile Val Gly Phe Ala Ile Glu Trp Gly Arg
20 25 30

Tyr Lys Glu Leu Phe Leu Ser Phe Glu Val Leu Glu Ile Leu Ser Val
35 40 45

Leu Phe Trp Phe Ile Gly Val Gly Met Ile Phe Ser Val Ile Ala Gln
50 55 60

Met Gly Phe Val Ile Phe Leu Thr Ile His Arg Phe Ala Leu Glu Ile
65 70 75 80

Phe Arg Ser His Ser Leu Trp Asn Ser Ile Gln Leu Phe Leu Ile Ile
85 90 95

Phe Val Ala Phe Asp Leu Val Tyr Leu Arg Phe Leu Phe Phe Glu Lys
100 105 110

Asp Gly Gly Ser Ile Ile Pro Tyr Ile Trp Leu Pro Leu Phe Ile Leu
115 120 125

Ala Val Gly Ile Ala Ala Ala Tyr Ala Lys Gln Lys Gln Ser Ser Lys
130 135 140

Lys Thr Phe Val Ser Ala Leu Phe Leu Met Phe Val Phe Thr Val Met
145 150 155 160

Glu Trp Phe Pro Ala Leu Arg Val Asn Glu Glu Asp Trp Leu Tyr Leu
165 170 175

Met Leu Leu Pro Leu Leu Ala Cys Asn Ala Phe Gln Leu Leu Met Leu
Page 30

10295.204.ST25.txt
185

180

190

Pro Lys Phe Gln Ala Arg Ala
195

<210> 27
 <211> 1991
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (489)..(1499)

<400> 27
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 gatcagcgca cgggtggaaat tccggtttgt tacggcggcc gtttcggccc tgatttggaag 120
 gaagtggccg acatcaacgg cctgactgca caggaagtca tcgatattca cacctcgggt 180
 gagtacctcg tttatatgat cggctttgcg ccgggcttcc cttacctagg cggaatgtct 240
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 ggaatagccg gcatgcaaac aggcgtctat cccctttcaa cgccgggagg ctggcagctg 360
 atcggcaata cgccgcttga attattcaag ctttatgaac agcctccgag ctttctgaga 420
 gcaggggata tcgtgaaatt tgtcagcgtg acagaagagg agtatcacgc gctgaaggag 480
 gggaaatc ttg agc ata gaa gtg tta aag ccg ggt ctg atg aca acg gtt 530
 Leu Ser Ile Glu Val Leu Lys Pro Gly Leu Met Thr Thr Val
 1 5 10
 caa gac ttg ggc cgc aca ggt ttt caa aaa tac ggc gtg ctt gtc agc 578
 Gln Asp Leu Gly Arg Thr Gly Phe Gln Lys Tyr Gly Val Leu Val Ser
 15 20 25 30
 ggt gcc atg gat gcc gat tct ttg cgg att gcc aat ctg ctc gcg ggg 626
 Gly Ala Met Asp Ala Asp Ser Leu Arg Ile Ala Asn Leu Leu Ala Gly
 35 40 45
 aac agc cag aac gaa gct gcg ctt gaa gtg acg ctg atg ggg ccg ggg 674
 Asn Ser Gln Asn Glu Ala Ala Leu Glu Val Thr Leu Met Gly Pro Gly
 50 55 60
 ccg tct ctc cgc ttt caa aaa cct gct ctt ata gcg gtg acg ggc gct 722
 Pro Ser Leu Arg Phe Gln Lys Pro Ala Leu Ile Ala Val Thr Gly Ala
 65 70 75
 gac ttt tca ctg atg gta aat gac gaa gaa gtc ccg ctt tgg cgc ccg 770
 Asp Phe Ser Leu Met Val Asn Asp Glu Glu Val Pro Leu Trp Arg Pro
 80 85 90
 gtt ttc atc aaa gag ggc agc gtg ttg aca ttc ggc atg tgc aag cgc 818
 Val Phe Ile Lys Glu Gly Ser Val Leu Thr Phe Gly Met Cys Lys Arg
 95 100 105 110
 gga agc cgt gca tat atg gca gtg gcc ggg gga att gat gtg ccg cct 866
 Gly Ser Arg Ala Tyr Met Ala Val Ala Gly Gly Ile Asp Val Pro Pro
 115 120 125
 gta atg gaa agc aaa agc aca tat gtc aga gca gga ctc ggc ggc ttt 914
 Val Met Glu Ser Lys Ser Thr Tyr Val Arg Ala Gly Leu Gly Gly Phe

10295.204.ST25.txt

130	135	140	
caa gga agg gcg ctt caa aag gga gac gtg tta tcg cta ggc agc ccg Gln Gly Arg Ala Leu Gln Lys Gly Asp Val Leu Ser Leu Gly Ser Pro 145 150 155			962
acg ccg ttg tcg gaa gcg ctg cac aga aag ctc gca gac gag ggc aaa Thr Pro Leu Ser Glu Ala Leu His Arg Lys Leu Ala Asp Glu Gly Lys 160 165 170			1010
gaa cgg ggc ttt gcg gct ccg aag tgg gct gtc gac cgc aaa tat ttt Glu Arg Gly Phe Ala Ala Pro Lys Trp Ala Val Asp Arg Lys Tyr Phe 175 180 185 190			1058
ctc ccg cta aaa aag aac ccg gtc att cgt gtc atc aaa ggc gat cag Leu Pro Leu Lys Lys Asn Pro Val Ile Arg Val Ile Lys Gly Asp Gln 195 200 205			1106
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ttc cgg gtg acg gct aaa tcc gac cgg atg ggg tac cgt ctt caa gga Phe Arg Val Thr Ala Lys Ser Asp Arg Met Gly Tyr Arg Leu Gln Gly 225 230 235			1202
gag gcg ctc gaa ctc act cag cct ctg gaa atg atc tct gaa gcg gta Glu Ala Leu Glu Leu Thr Gln Pro Leu Glu Met Ile Ser Glu Ala Val 240 245 250			1250
tca ttc gga acg att caa gtg ccg ccc gac ggc aat ccg atc gtt ctt Ser Phe Gly Thr Ile Gln Val Pro Pro Asp Gly Asn Pro Ile Val Leu 255 260 265 270			1298
ctc gca gac agg cag aca gcg ggc gga tac ccg aga atc gcc cat atc Leu Ala Asp Arg Gln Thr Ala Gly Gly Tyr Pro Arg Ile Ala His Ile 275 280 285			1346
gca tca gct gat ttt tct cag gtc acg cag atg atg ccg ggc gag cag Ala Ser Ala Asp Phe Ser Gln Val Thr Gln Met Met Pro Gly Glu Gln 290 295 300			1394
gtg cag ttt cag ctt gtc agc ctt cag gaa gca gag cgc gtt tac atc Val Gln Phe Gln Leu Val Ser Leu Gln Glu Ala Glu Arg Val Tyr Ile 305 310 315			1442
gaa cgg gag acg aaa atc agc gaa ctt tct gcc cga ttg aag ctt gaa Glu Arg Glu Thr Lys Ile Ser Glu Leu Ser Ala Arg Leu Lys Leu Glu 320 325 330			1490
tac atg tta tgataggtgt gatgtgtatc aggaggggga aggcattggaa Tyr Met Leu 335			1539
cataaaaaaca aaacagtcgt caaagccatg accctgctca atctgttcct gacgagagaa			1599
aggctctcgc tgggcgacat gattgagctg acaggcatgc cgaaaacatc tgtctaccgc			1659
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gtaaggcagg gaaatgaagc aatgtatata gaaaaaattg agggcacgca gaccgttcgc			1899
ctctatacag cgatcgggag gcggtcccct ttatatgccg gagcctgtgc gagaagcatt			1959

10295.204.ST25.txt

1991

ctgacgtttt tgcctgaaga ggagcgggat gc

<210> 28
 <211> 337
 <212> PRT
 <213> Bacillus licheniformis

<400> 28

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 20 25 30

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 35 40 45

Gln Asn Glu Ala Ala Leu Glu Val Thr Leu Met Gly Pro Gly Pro Ser
 50 55 60

Leu Arg Phe Gln Lys Pro Ala Leu Ile Ala Val Thr Gly Ala Asp Phe
 65 70 75 80

Ser Leu Met Val Asn Asp Glu Glu Val Pro Leu Trp Arg Pro Val Phe
 85 90 95

Ile Lys Glu Gly Ser Val Leu Thr Phe Gly Met Cys Lys Arg Gly Ser
 100 105 110

Arg Ala Tyr Met Ala Val Ala Gly Gly Ile Asp Val Pro Pro Val Met
 115 120 125

Glu Ser Lys Ser Thr Tyr Val Arg Ala Gly Leu Gly Gly Phe Gln Gly
 130 135 140

Arg Ala Leu Gln Lys Gly Asp Val Leu Ser Leu Gly Ser Pro Thr Pro
 145 150 155 160

Leu Ser Glu Ala Leu His Arg Lys Leu Ala Asp Glu Gly Lys Glu Arg
 165 170 175

Gly Phe Ala Ala Pro Lys Trp Ala Val Asp Arg Lys Tyr Phe Leu Pro
 180 185 190

Leu Lys Lys Asn Pro Val Ile Arg Val Ile Lys Gly Asp Gln Phe Ala
 195 200 205

Cys Phe Thr Ser Ser Ser Gln Glu Arg Phe Phe Ala Gly Pro Phe Arg
 210 215 220

Val Thr Ala Lys Ser Asp Arg Met Gly Tyr Arg Leu Gln Gly Glu Ala
 225 230 235 240

10295.204.ST25.txt

Leu Glu Leu Thr Gln Pro Leu Glu Met Ile Ser Glu Ala Val Ser Phe
 245 250 255

Gly Thr Ile Gln Val Pro Pro Asp Gly Asn Pro Ile Val Leu Leu Ala
 260 265 270

Asp Arg Gln Thr Ala Gly Gly Tyr Pro Arg Ile Ala His Ile Ala Ser
 275 280 285

Ala Asp Phe Ser Gln Val Thr Gln Met Met Pro Gly Glu Gln Val Gln
 290 295 300

Phe Gln Leu Val Ser Leu Gln Glu Ala Glu Arg Val Tyr Ile Glu Arg
 305 310 315 320

Glu Thr Lys Ile Ser Glu Leu Ser Ala Arg Leu Lys Leu Glu Tyr Met
 325 330 335

Leu

<210> 29
 <211> 2287
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 <222> (501)..(1784)

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 tatgagctgc ttacatttaa ctggatggcc cattcgctga cgcttgaata tgaggtgatc 180
 ggtcaagtca aggatttgct agcttatgaa gaaaggctcg tcgttctcat cagaaagctg 240
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 cagacggacg gtccggacga ccgcctcgct atctttctcg atttccacgg cgtattcaca 360
 aagctgaccg gtatcaaaga ctttcatcat tctaggccg acttttatga aatcaagcgg 420
 ttgatgtaa cagaccgtga gtgcatcgcc gaaattcata tcaagtaaag cgttttttta 480
 ggaatagaac ggaggacatt atg ttt gtt gat cag gtg aaa ata tac gta aaa 533
 Met Phe Val Asp Gln Val Lys Ile Tyr Val Lys
 1 5 10
 ggc gga gac gga ggc aac ggt atg gtt gct ttc cgc cgc gaa aaa tat 581
 Gly Gly Asp Gly Gly Asn Gly Met Val Ala Phe Arg Arg Glu Lys Tyr
 15 20 25
 gtg cca aaa gga ggc cct gcc gga ggt gac ggc gga aaa ggc gga gac 629
 Val Pro Lys Gly Gly Pro Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp
 30 35 40

10295.204.ST25.txt

gtc gtt ttc aaa gtt gac gaa ggt ctc agc acg ctg atg gat ttt aga Val Val Phe Lys Val Asp Glu Gly Leu Ser Thr Leu Met Asp Phe Arg 45 50 55	677
tat caa aga cat ttt aag gca gcg cgc gga gaa cac ggc atg tct aaa Tyr Gln Arg His Phe Lys Ala Ala Arg Gly Glu His Gly Met Ser Lys 60 65 70 75	725
aac cag cac ggc cga aat gcc gaa gac atg gtt gtg aaa gtc ccg ccc Asn Gln His Gly Arg Asn Ala Glu Asp Met Val Val Lys Val Pro Pro 80 85 90	773
ggc acg gtt gtc att gac gat gat aca aaa cag gtc atc gct gat tta Gly Thr Val Val Ile Asp Asp Asp Thr Lys Gln Val Ile Ala Asp Leu 95 100 105	821
acg gag cac gga cag gaa gcc gtc atc gca aaa ggc gga cgc ggc gga Thr Glu His Gly Gln Glu Ala Val Ile Ala Lys Gly Gly Arg Gly Gly 110 115 120	869
cgg ggc aat aca cgt ttt gcg acg cct gcc aac ccg gcg ccg cag ctt Arg Gly Asn Thr Arg Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu 125 130 135	917
tct gaa aac ggc gaa ccc ggc aag gag cgc tat att gtt ctc gag ctg Ser Glu Asn Gly Glu Pro Gly Lys Glu Arg Tyr Ile Val Leu Glu Leu 140 145 150 155	965
aaa gtt ttg gca gat gtc ggt ctt gtc ggc ttc cca agc gtc gga aaa Lys Val Leu Ala Asp Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys 160 165 170	1013
tca acg ctc ctg tct gtc gtg tct tcg gcc aag ccg aaa att gcc gat Ser Thr Leu Leu Ser Val Val Ser Ser Ala Lys Pro Lys Ile Ala Asp 175 180 185	1061
tac cac ttt aca acg ctg aac ccg aat ctc gga atg gtc gaa acg gaa Tyr His Phe Thr Thr Leu Asn Pro Asn Leu Gly Met Val Glu Thr Glu 190 195 200	1109
gac ggc cgc agc ttt gta atg gcg gat ctt ccg gga ctg att gag ggc Asp Gly Arg Ser Phe Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly 205 210 215	1157
gcg cac gaa gga gtt ggc ctc gga cac caa ttc ctc agg cat atc gaa Ala His Glu Gly Val Gly Leu Gly His Gln Phe Leu Arg His Ile Glu 220 225 230 235	1205
aga acg cgc gtc atc gtg cac gtt att gac atg tcg ggt ctt gaa ggc Arg Thr Arg Val Ile Val His Val Ile Asp Met Ser Gly Leu Glu Gly 240 245 250	1253
cgc gac ccg tat gaa gat tat gtg acc att aat aaa gag ctt gaa cag Arg Asp Pro Tyr Glu Asp Tyr Val Thr Ile Asn Lys Glu Leu Glu Gln 255 260 265	1301
tat aat ctc agg ctg aca gaa cgt cct caa att att gtc gcc aat aaa Tyr Asn Leu Arg Leu Thr Glu Arg Pro Gln Ile Ile Val Ala Asn Lys 270 275 280	1349
atg gat atg ccg gat gcg gaa gaa aat ctg aag gct ttc aaa gaa aag Met Asp Met Pro Asp Ala Glu Glu Asn Leu Lys Ala Phe Lys Glu Lys 285 290 295	1397
ctc aca gat gat tat cct gtt ttt cca atc agc gcg gtg acc aga caa Leu Thr Asp Asp Tyr Pro Val Phe Pro Ile Ser Ala Val Thr Arg Gln 300 305 310 315	1445

10295.204.ST25.txt

ggc ttg agg gat ctg ctg ttt gaa att gcc gac cgt ttg gaa acg acg 1493
 Gly Leu Arg Asp Leu Leu Phe Glu Ile Ala Asp Arg Leu Glu Thr Thr
 320 325 330

ccg gaa ttc ccg ctc tac gac gaa gaa gac atg gct gaa aac aga gtc 1541
 Pro Glu Phe Pro Leu Tyr Asp Glu Glu Asp Met Ala Glu Asn Arg Val
 335 340 345

atg tat aag ctt gag gat gag gaa gcg ccg ttt gag atc agc cgt gat 1589
 Met Tyr Lys Leu Glu Asp Glu Glu Ala Pro Phe Glu Ile Ser Arg Asp
 350 355 360

cct gac ggc acc ttc gtg ctc agc gga gcc aag ctt gaa cgc tta ttt 1637
 Pro Asp Gly Thr Phe Val Leu Ser Gly Ala Lys Leu Glu Arg Leu Phe
 365 370 375

aaa atg acg gac ttt tca aga gat gag tct gtt aag cgt ttt gcc aga 1685
 Lys Met Thr Asp Phe Ser Arg Asp Glu Ser Val Lys Arg Phe Ala Arg
 380 385 390 395

cag ctt cgc gga atg ggc gtc gat gat gcg ctt cgg gcc cgc ggt gca 1733
 Gln Leu Arg Gly Met Gly Val Asp Asp Ala Leu Arg Ala Arg Gly Ala
 400 405 410

aaa gac ggg gat acg atc cgt ctt ctc gaa ttt gaa ttt gaa ttt atc 1781
 Lys Asp Gly Thr Ile Arg Leu Leu Glu Phe Glu Phe Glu Phe Ile
 415 420 425

gac tgatcatacc ggagagtttg ccaagcaagc tctccgactt ttagctgaaa 1834
 Asp

ggaacgccct tcctttcgca ggatcaatgt aaaggaatca gggtttttaa aaggagagaa 1894
 aagtctgtga aagaggagac cttttatctt gtcagggaag acgtgctgcc ggaggcaatg 1954
 cggaacacac ttgaggtcaa aaagctgatt gagcggaaaa aagcggaatc tgtagctgaa 2014
 gccgtacaaa aggtagatatt gagccgaagc gctttttata agtacagaga tgcgggttttt 2074
 cctttttata cgatgggtcaa ggaacagatt atcacgcttt tttttcattt ggaggaccgc 2134
 tcaggaacgc tgtcccatct gctgcaagtg gtagctgaat cgggctgcaa tgtgctgtcg 2194
 atccaccaga ccatccctct tcaaggaaga gcgaatgtca cgctctctgt cagtacgaga 2254
 ggcatggatg aaaatatcga tttgctgatg aac 2287

<210> 30
 <211> 428
 <212> PRT
 <213> Bacillus licheniformis

<400> 30

Met Phe Val Asp Gln Val Lys Ile Tyr Val Lys Gly Gly Asp Gly Gly
 1 5 10 15

Asn Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Lys Gly Gly
 20 25 30

Pro Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp Val Val Phe Lys Val
 35 40 45

10295.204.ST25.txt

Asp Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe
 50 55 60
 Lys Ala Ala Arg Gly Glu His Gly Met Ser Lys Asn Gln His Gly Arg
 65 70 75 80
 Asn Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile
 85 90 95
 Asp Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln
 100 105 110
 Glu Ala Val Ile Ala Lys Gly Gly Arg Gly Gly Arg Gly Asn Thr Arg
 115 120 125
 Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu
 130 135 140
 Pro Gly Lys Glu Arg Tyr Ile Val Leu Glu Leu Lys Val Leu Ala Asp
 145 150 155 160
 Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Ser
 165 170 175
 Val Val Ser Ser Ala Lys Pro Lys Ile Ala Asp Tyr His Phe Thr Thr
 180 185 190
 Leu Asn Pro Asn Leu Gly Met Val Glu Thr Glu Asp Gly Arg Ser Phe
 195 200 205
 Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly Ala His Glu Gly Val
 210 215 220
 Gly Leu Gly His Gln Phe Leu Arg His Ile Glu Arg Thr Arg Val Ile
 225 230 235 240
 Val His Val Ile Asp Met Ser Gly Leu Glu Gly Arg Asp Pro Tyr Glu
 245 250 255
 Asp Tyr Val Thr Ile Asn Lys Glu Leu Glu Gln Tyr Asn Leu Arg Leu
 260 265 270
 Thr Glu Arg Pro Gln Ile Ile Val Ala Asn Lys Met Asp Met Pro Asp
 275 280 285
 Ala Glu Glu Asn Leu Lys Ala Phe Lys Glu Lys Leu Thr Asp Asp Tyr
 290 295 300
 Pro Val Phe Pro Ile Ser Ala Val Thr Arg Gln Gly Leu Arg Asp Leu
 305 310 315 320

10295.204.ST25.txt

Leu Phe Glu Ile Ala Asp Arg Leu Glu Thr Thr Pro Glu Phe Pro Leu
 325 330 335

Tyr Asp Glu Glu Asp Met Ala Glu Asn Arg Val Met Tyr Lys Leu Glu
 340 345 350

Asp Glu Glu Ala Pro Phe Glu Ile Ser Arg Asp Pro Asp Gly Thr Phe
 355 360 365

Val Leu Ser Gly Ala Lys Leu Glu Arg Leu Phe Lys Met Thr Asp Phe
 370 375 380

Ser Arg Asp Glu Ser Val Lys Arg Phe Ala Arg Gln Leu Arg Gly Met
 385 390 395 400

Gly Val Asp Asp Ala Leu Arg Ala Arg Gly Ala Lys Asp Gly Asp Thr
 405 410 415

Ile Arg Leu Leu Glu Phe Glu Phe Glu Phe Ile Asp
 420 425

<210> 31
 <211> 2115
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1616)

<400> 31
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 atgtgatgcc ctcaacagcc tttttgactt tggcgatttc gtctgattgt tgttttaatt 120
 gttccagcgt ttgatctatt gcattgtgca gcgcctgaac atcaagagtc ttcattggcat 180
 tctcctctaa tccttttcat tacaatcagt atatagtta ccactttata gaaagtactt 240
 ggtgaatata tcctgttcaa ccatgaaaat gaatcattgg gcttaggtca ttattttctat 300
 tgattcattt cgattaccgt aaacaagttt gttgtagcat tctttaggct ctgtgactaa 360
 accaaaaagc catttgtttt aaattggctt ttcggtatca cgaaaatttc gttttttggg 420
 ctgatagaag ttttgcaatt atgaattgta tgtaaatctt taacataaaa aggatgtag 480
 ctggaaggga atgatggcag ttg gag act atc ccg tct tca gaa gtt gga atc 533
 Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile
 1 5 10
 aaa ata aac cgc tgg tac aac gaa att caa aaa tta aac gta ata gaa 581
 Lys Ile Asn Arg Trp Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu
 15 20 25
 gca gaa cga tta aag gcg gaa gtt cac tta gct ata gaa aga atg gaa 629
 Ala Glu Arg Leu Lys Ala Glu Val His Leu Ala Ile Glu Arg Met Glu
 30 35 40

10295.204.ST25.txt

gaa gat cag gac ttg ctt tcc tat tat cag ctt atg aat ttt aga cat Glu Asp Gln Asp Leu Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His 45 50 55	677
gag tta atg ttg gaa tat ctt ttc ccg gca gaa aaa aag ctg agc aaa Glu Leu Met Leu Glu Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys 60 65 70 75	725
tct gat tat ctt agg gaa att gag gga cag gga aga aaa ttg tca ggc Ser Asp Tyr Leu Arg Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly 80 85 90	773
ttg ctc gaa tac tat ttt tcc ttt ttc acc gga atg tat cat ttt tct Leu Leu Glu Tyr Tyr Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser 95 100 105	821
cgc gga aaa tac ata aag gca atc aag gca tat aga gca gca gaa aaa Arg Gly Lys Tyr Ile Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys 110 115 120	869
aag ttg acg aaa gtt tca gat aaa ata gaa aag gct gaa ttc tat tat Lys Leu Thr Lys Val Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr 125 130 135	917
aag atg gcg gaa gtg ttt tat cat atg aaa cag act cat atg tca atg Lys Met Ala Glu Val Phe Tyr His Met Lys Gln Thr His Met Ser Met 140 145 150 155	965
tat tat gtg tct ctc gct tat gat att tat aaa tcc tat gat gca tat Tyr Tyr Val Ser Leu Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr 160 165 170	1013
gtg att cga aga att aat tgt cta ttc gtt gtt gct ggg aat tac att Val Ile Arg Arg Ile Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile 175 180 185	1061
gat tta tca acc cat gat caa gct tta ccg cat ctt tta agc gct aag Asp Leu Ser Thr His Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys 190 195 200	1109
gaa tcc gcg gaa gac att caa aac aag gcg atc gtt gca aag gct ctt Glu Ser Ala Glu Asp Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu 205 210 215	1157
tta aat gta gca tat tgt tat aat gca atg gag aga cca aca aaa gct Leu Asn Val Ala Tyr Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala 220 225 230 235	1205
att gaa tac ttt cat aag gcg att gat gta gca aag gaa ata aag gca Ile Glu Tyr Phe His Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala 240 245 250	1253
aaa gaa ctg act cag gct tat tat gat ttg gca tta att cac ttt cga Lys Glu Leu Thr Gln Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg 255 260 265	1301
aat aac gaa aat att gaa gga cga aaa ttt tat gaa aag gcg ctt gaa Asn Asn Glu Asn Ile Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu 270 275 280	1349
agt gcg ccg gta ttt gaa gat gaa tta ttc ctg tgt ctg ttg gat gtt Ser Ala Arg Val Phe Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val 285 290 295	1397
tta gag gca ctg ttt ata aaa tca gct aat aag tca gag gta cta gaa Leu Glu Ala Leu Phe Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu 300 305 310 315	1445

10295.204.ST25.txt

aca atg aaa cca tta cgg gat agt cgt ggt tac ccc tat ctt gag gaa 1493
 Thr Met Lys Pro Leu Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu
 320 325 330
 ctg gca tta gaa gca gct cta ttc tat act agg aat gag cgg cca aat 1541
 Leu Ala Leu Glu Ala Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn
 335 340 345
 gat tcc ata ttt ttt tat gat cag atg gtg cag gct cag aaa caa atc 1589
 Asp Ser Ile Phe Phe Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile
 350 355 360
 aaa agg ggc gac ttt ctg tat gaa atc taagctgttt ctttcgctga 1636
 Lys Arg Gly Asp Phe Leu Tyr Glu Ile
 365 370
 cccttgcttt gggcttggtt gtcgtgtcga gcgcttccat tcacacatct gttgaacaac 1696
 aacatgcaga attttctgta gcatctaggc tcgcaacata attgtgtttt ggcagggtcat 1756
 gtgatggcct gccttttttg tgaaagaatt attttagttt gaaaaccaga acgattgtgt 1816
 taatactcat ctttcttcgt cccttggtgtt ggaattttca tcatatcaat atttgaatat 1876
 gcggctgtcc gcattattaa caattttaaa tttttgcac aaattttata caaaggcaga 1936
 caaaaacctt gatatatcaa tggttctatg ggtatattca accacgacca ccgatatcgc 1996
 taaaaaccgt attgccaaac gacgaaagag cgttccttac acaaggaatg ctctttttgt 2056
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<210> 32
 <211> 372
 <212> PRT
 <213> Bacillus licheniformis
 <400> 32

Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile Lys Ile Asn Arg Trp
 1 5 10 15

Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu Ala Glu Arg Leu Lys
 20 25 30

Ala Glu Val His Leu Ala Ile Glu Arg Met Glu Glu Asp Gln Asp Leu
 35 40 45

Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His Glu Leu Met Leu Glu
 50 55 60

Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys Ser Asp Tyr Leu Arg
 65 70 75 80

Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly Leu Leu Glu Tyr Tyr
 85 90 95

Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser Arg Gly Lys Tyr Ile
 100 105 110

10295.204.ST25.txt

Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys Lys Leu Thr Lys Val
 115 120 125
 Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr Lys Met Ala Glu Val
 130 135 140
 Phe Tyr His Met Lys Gln Thr His Met Ser Met Tyr Tyr Val Ser Leu
 145 150 155 160
 Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr Val Ile Arg Arg Ile
 165 170 175
 Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile Asp Leu Ser Thr His
 180 185 190
 Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys Glu Ser Ala Glu Asp
 195 200 205
 Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu Leu Asn Val Ala Tyr
 210 215 220
 Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala Ile Glu Tyr Phe His
 225 230 235 240
 Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala Lys Glu Leu Thr Gln
 245 250 255
 Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg Asn Asn Glu Asn Ile
 260 265 270
 Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu Ser Ala Arg Val Phe
 275 280 285
 Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val Leu Glu Ala Leu Phe
 290 295 300
 Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu Thr Met Lys Pro Leu
 305 310 315 320
 Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu Leu Ala Leu Glu Ala
 325 330 335
 Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn Asp Ser Ile Phe Phe
 340 345 350
 Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile Lys Arg Gly Asp Phe
 355 360 365
 Leu Tyr Glu Ile
 370

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<210> 33
<211> 2077
<212> DNA
<213> Bacillus licheniformis
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<220>
<221> CDS
<222> (501) .. (1574)

[illegible]

10295.204.ST25.txt

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 aat tat att gac caa ttt aag ttt gcc gaa agt gaa gta ttg tta aag 1061
 Asn Tyr Ile Asp Gln Phe Lys Phe Ala Glu Ser Glu Val Leu Leu Lys
 175 180 185
 gaa gca att gaa aaa acc gaa aaa atc ggc gac caa tat ctt ttg cct 1109
 Glu Ala Ile Glu Lys Thr Glu Lys Ile Gly Asp Gln Tyr Leu Leu Pro
 190 200
 tat acc tac tat aat atg ggc ttt ttg aag agt aag gaa gat aaa cac 1157
 Tyr Thr Tyr Tyr Asn Met Gly Phe Leu Lys Ser Lys Glu Asp Lys His
 205 210 215
 gaa gaa gcg ctg aag tat tat aat aaa gct ttt gca atc aaa gac ttt 1205
 Glu Glu Ala Leu Lys Tyr Tyr Asn Lys Ala Phe Ala Ile Lys Asp Phe
 220 225 230 235
 gaa acg aaa gcc aag tat gct tac ctt cta tgt gta tat gaa aac aca 1253
 Glu Thr Lys Ala Lys Tyr Ala Tyr Leu Leu Cys Val Tyr Glu Asn Thr
 240 245 250
 agg tct ctt ttc aaa acc aac gat ccc gac caa gct ttt aaa tgg atc 1301
 Arg Ser Leu Phe Lys Thr Asn Asp Pro Asp Gln Ala Phe Lys Trp Ile
 255 260 265
 gac aca ggc ttt aaa aaa gct caa gaa gtg aat agc gaa att ttc gaa 1349
 Asp Thr Gly Phe Lys Lys Ala Gln Glu Val Asn Ser Glu Ile Phe Glu
 270 275 280
 tta aaa ttc aaa act tta tat aca tta cat tcc gat tgt cag aat aaa 1397
 Leu Lys Phe Lys Thr Leu Tyr Thr Leu His Ser Asp Cys Gln Asn Lys
 285 290 295
 ctg gaa gta atc aag gac ttt att cac caa tta gaa gat aaa aaa gca 1445
 Leu Glu Val Ile Lys Asp Phe Ile His Gln Leu Glu Asp Lys Lys Ala
 300 305 310 315
 tgg gtt gat ctg gag gaa ttg ctg atg gac gta gcg aat tac tat agg 1493
 Trp Val Asp Leu Glu Glu Leu Leu Met Asp Val Ala Asn Tyr Tyr Arg
 320 325 330
 gaa aat aag tta tac gaa gaa gcc ata tat ttc tac att aaa aca gac 1541
 Glu Asn Lys Leu Tyr Glu Glu Ala Ile Tyr Phe Tyr Ile Lys Thr Asp
 335 340 345
 aag gca agt aaa ctt gcc gga aga gga gga gaa taggatgaaa aaagtgttgt 1594
 Lys Ala Ser Lys Leu Ala Gly Arg Gly Gly Glu
 350
 tagctgtatt tgtattaggc actgttttca gcttttcgtt tgcaaatacac gctcctgaag 1654
 cggttccca aagcaatgag atacttttgg cttctcgtgg agcaggcggg tgactacatc 1714
 ctcaaaatac ccattcagac atctgctgaa tgggtatttt gcactttaca ttcattattca 1774
 ggagtgatcg atatgggaaa gaaagtactg ctgacaggat ttgaccctt tgggggagaa 1834
 acagtcaatc cgtcctggga agctgtaaaa cggtgaaacg gagaggaagc agaaggcgtc 1894
 tctatcgag cggagcagat tccgaccgtt tttcatcatt cagcggccgt tttgaaaaaa 1954
 gcgatcgaaa agcacaaacc cgatgtcgtc atttgcgag ggcaagcagg cggcagggct 2014
 catattacgc cggaacgcat cgcaatcaac atcgatgatg ctgcattcc ggataatgaa 2074
 gac 2077

10295.204.ST25.txt

<210> 34
 <211> 358
 <212> PRT
 <213> Bacillus licheniformis

<400> 34

Met Leu Asn Asp Trp Tyr Ile Leu Met Lys Lys Arg Asp Ile Ser Gly
 1 5 10 15

Ser Ile Glu Met Lys Asp Asp Ile Asp Lys Ala Ile Glu Lys Met Glu
 20 25 30

Glu Asp His Asp Val Leu Leu Tyr Tyr Gln Met Leu Asp Phe Arg Leu
 35 40 45

Arg Leu Leu Leu Glu Asp Ile Ser Gln Ser Ser Thr Glu Lys Leu Glu
 50 55 60

Ala Ile Ser Phe Lys Asp Lys Asp Pro Lys Ser Thr Asp Asp Lys Leu
 65 70 75 80

Asn Tyr Tyr Phe Tyr Leu Phe Lys Gly Ile Tyr Glu Asp Tyr Lys Gln
 85 90 95

Asn His Thr Glu Ala Leu Asn Phe Phe Arg Ile Ala Glu Lys Arg Leu
 100 105 110

Ser Val Ile Gln Asn Glu Ile Glu Lys Ala Glu Phe His Tyr Lys Ile
 115 120 125

Gly Val Leu Tyr Tyr Asn Leu Lys Ala Thr Trp Leu Ser Ile His His
 130 135 140

Ile Asn Ile Ala Ser Gly Ile Phe Gln Gly Tyr Asp Gly Tyr Ala Lys
 145 150 155 160

Arg Val Ile Asn Cys Lys Met Leu Ile Gly Leu Asn Tyr Ile Asp Gln
 165 170 175

Phe Lys Phe Ala Glu Ser Glu Val Leu Leu Lys Glu Ala Ile Glu Lys
 180 185 190

Thr Glu Lys Ile Gly Asp Gln Tyr Leu Leu Pro Tyr Thr Tyr Tyr Asn
 195 200 205

Met Gly Phe Leu Lys Ser Lys Glu Asp Lys His Glu Glu Ala Leu Lys
 210 215 220

Tyr Tyr Asn Lys Ala Phe Ala Ile Lys Asp Phe Glu Thr Lys Ala Lys
 225 230 235 240

10295.204.ST25.txt

Tyr Ala Tyr Leu Leu Cys Val Tyr Glu Asn Thr Arg Ser Leu Phe Lys
245 250 255

Thr Asn Asp Pro Asp Gln Ala Phe Lys Trp Ile Asp Thr Gly Phe Lys
260 265 270

Lys Ala Gln Glu Val Asn Ser Glu Ile Phe Glu Leu Lys Phe Lys Thr
275 280 285

Leu Tyr Thr Leu His Ser Asp Cys Gln Asn Lys Leu Glu Val Ile Lys
290 295 300

Asp Phe Ile His Gln Leu Glu Asp Lys Lys Ala Trp Val Asp Leu Glu
305 310 315 320

Glu Leu Leu Met Asp Val Ala Asn Tyr Tyr Arg Glu Asn Lys Leu Tyr
325 330 335

Glu Glu Ala Ile Tyr Phe Tyr Ile Lys Thr Asp Lys Ala Ser Lys Leu
340 345 350

Ala Gly Arg Gly Gly Glu
355

<210> 35
<211> 2101
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1598)

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gcatatttga aaagaaacac agacggaaaa gaactgagct gcagcccggc tggaggaaaa 120
ggaaaagtgc tcccggggca gacatcctgt tatacaccga tggttgattt cgatccgcgt 180
tcttcatatg cgatgtagaa acattatcaa tccattaaca ggagctctca cttattccta 240
tacaagttcg tattcatatt tgaagaagta gtgtataaaa gcaccctttc agcaaggggtg 300
ctttttgctg tcttatcagt cacggtttca cagctattga agagtcattt gacctaataa 360
aagagtggga aaagtggggg attcaggaaa ctgtgtaaaa tgaactatta ctattaattt 420
atacagggag gaaaatatag tatgatatga ataatgaata aaatacaaaa aaattgaata 480
tcggaagaaa ggagctccat atg aac aag atc gcc gcg gaa gaa gtc gcc aac 533
Met Asn Lys Ile Ala Ala Glu Glu Val Ala Asn
1 5 10
atc ctt aat aca tgg tac cgc gcc atc aga aga aat gat gct gaa cag 581
Ile Leu Asn Thr Trp Tyr Arg Ala Ile Arg Arg Asn Asp Ala Glu Gln
15 20 25

10295.204.ST25.txt

tcg atc cga ata ttt gaa gaa gtc aaa ccg atg ctg gca gag atg gag Ser Ile Arg Ile Phe Glu Glu Val Lys Pro Met Leu Ala Glu Met Glu 30 35 40	629
gaa gac caa gag gtt tta atc tac tat tct ctg ctg gaa ctg cgg cat Glu Asp Gln Glu Val Leu Ile Tyr Tyr Ser Leu Leu Glu Leu Arg His 45 50 55	677
aaa atc atg ctg tat gat acg cgg gga aaa aag ata gaa cag caa gag Lys Ile Met Leu Tyr Asp Thr Arg Gly Lys Lys Ile Glu Gln Gln Glu 60 65 70 75	725
gag tta acg aac ggc ggc agt gct gca tca cat atg aca tcc tat tac Glu Leu Thr Asn Gly Gly Ser Ala Ala Ser His Met Thr Ser Tyr Tyr 80 85 90	773
tac tac ctg ttt tca gga gct tat gaa gtg tat aaa aag aat tat gag Tyr Tyr Leu Phe Ser Gly Ala Tyr Glu Val Tyr Lys Lys Asn Tyr Glu 95 100 105	821
cag gcg atc agc ttc tat aaa att gcc gag aag aag ctt gct cat gta Gln Ala Ile Ser Phe Tyr Lys Ile Ala Glu Lys Lys Leu Ala His Val 110 115 120	869
cat gat gaa att gag gtg gcg caa ttt cac gat aaa gtc gga aag ctc His Asp Glu Ile Glu Val Ala Gln Phe His Asp Lys Val Gly Lys Leu 125 130 135	917
tac tat tac ttg ggc cag aat atc gtc tct tta aac cat acc cgg cag Tyr Tyr Tyr Leu Gly Gln Asn Ile Val Ser Leu Asn His Thr Arg Gln 140 145 150 155	965
gcg atg gaa att ttc aag ggg cat ggc gac cat gat atg aac ctt gtt Ala Met Glu Ile Phe Lys Gly His Gly Asp His Asp Met Asn Leu Val 160 165 170	1013
tcc act tat att acg atg gcc gga aat tat aca gag atg ggg aaa tat Ser Thr Tyr Ile Thr Met Ala Gly Asn Tyr Thr Glu Met Gly Lys Tyr 175 180 185	1061
aca gag gcg gaa gaa tat tta aca gaa gcc atc cat acg gta aga aaa Thr Glu Ala Glu Glu Tyr Leu Thr Glu Ala Ile His Thr Val Arg Lys 190 195 200	1109
gcc gcc gac tgt ttt aaa gaa atg cag ctc ctt cat aat ttt gcc ttg Ala Gly Asp Cys Phe Lys Glu Met Gln Leu Leu His Asn Phe Ala Leu 205 210 215	1157
ctt tat gcg gcg atg gac aat tcg gaa aaa agc att cag ttt tta gaa Leu Tyr Ala Ala Met Asp Asn Ser Glu Lys Ser Ile Gln Phe Leu Glu 220 225 230 235	1205
atc gtt ttg gat gat caa gca tat gct gca tca gat tat tat ttc aat Ile Val Leu Asp Asp Gln Ala Tyr Ala Ala Ser Asp Tyr Tyr Phe Asn 240 245 250	1253
gct gtg ttt tta atg atc aaa gag ctg ttt aaa gtc gga gac cat aaa Ala Val Phe Leu Met Ile Lys Glu Leu Phe Lys Val Gly Asp His Lys 255 260 265	1301
cgc gct gca gcc ttt tac aaa gaa ggg aag gaa agg tcg aaa tcc gcg Arg Ala Ala Ala Phe Tyr Lys Glu Gly Lys Glu Arg Ser Lys Ser Ala 270 275 280	1349
gcg aat aaa ata ttt gac gcc aaa atc gat att tta tat gcg gct tat Ala Asn Lys Ile Phe Asp Ala Lys Ile Asp Ile Leu Tyr Ala Ala Tyr 285 290 295	1397

10295.204.ST25.txt

gca gga gat ggt gaa cag gcg gtt aaa gac tgc aaa gac aac att gaa 1445
 Ala Gly Asp Gly Glu Gln Ala Val Lys Asp Cys Lys Asp Asn Ile Glu
 300 305 310 315

atc ctg ttt caa aca aag caa tac gac agc gcc aga gaa ctt tcg ctc 1493
 Ile Leu Phe Gln Thr Lys Gln Tyr Asp Ser Ala Arg Glu Leu Ser Leu
 320 325 330

tta acg gcc aat gtt tac aga tca aag tca ctt tat aaa gaa gcc gca 1541
 Leu Thr Ala Asn Val Tyr Arg Ser Lys Ser Leu Tyr Lys Glu Ala Ala
 335 340 345

cat ttc ttt ttg gaa gcg att aaa gcg gaa gaa aaa atg aaa aaa gtg 1589
 His Phe Phe Leu Glu Ala Ile Lys Ala Glu Glu Lys Met Lys Lys Val
 350 355 360

gag gga atg tgatgaaaaa actgttcatt gttgctgcga ttgctgccgt 1638
 Glu Gly Met
 365

cgatatgttcg ggatgggtttg cggcagaaac tcaactgggca tccggcgaca tgcaggttgc 1698
 tgaaaagatg gtcgggttaaa tcgaatactc ggaacaaata tgaacatccg ctcttgagca 1758
 tcagggcgga tttttttggg aaggtaaagt aaattaaggc ataagaaacg cggttagaca 1818
 atgaacactt cttcaccact atttaggggtg gtcaacctaa acaaagggtac gaaacctgtg 1878
 ctgactactt ttactccgat gtcctttcag ctattcttgt cagtaagatc attccccatc 1938
 tcttcaacgc ctcaggcatc acctattaaa aaaatcataa ttgaaacttg tcagcaaata 1998
 tgttgcataa caccaggatg tttccacaat aattaaacat taagactttt ttgacttcca 2058
 gaaggaagaa caagatatat atgtaaaatc actcttttat tca 2101

<210> 36
 <211> 366
 <212> PRT
 <213> Bacillus licheniformis

<400> 36

Met Asn Lys Ile Ala Ala Glu Glu Val Ala Asn Ile Leu Asn Thr Trp
 1 5 10 15

Tyr Arg Ala Ile Arg Arg Asn Asp Ala Glu Gln Ser Ile Arg Ile Phe
 20 25 30

Glu Glu Val Lys Pro Met Leu Ala Glu Met Glu Glu Asp Gln Glu Val
 35 40 45

Leu Ile Tyr Tyr Ser Leu Leu Glu Leu Arg His Lys Ile Met Leu Tyr
 50 55 60

Asp Thr Arg Gly Lys Lys Ile Glu Gln Gln Glu Glu Leu Thr Asn Gly
 65 70 75 80

Gly Ser Ala Ala Ser His Met Thr Ser Tyr Tyr Tyr Tyr Leu Phe Ser
 85 90 95

10295.204.ST25.txt

Gly Ala Tyr Glu Val Tyr Lys Lys Asn Tyr Glu Gln Ala Ile Ser Phe
 100 105 110

Tyr Lys Ile Ala Glu Lys Lys Leu Ala His Val His Asp Glu Ile Glu
 115 120 125

Val Ala Gln Phe His Asp Lys Val Gly Lys Leu Tyr Tyr Tyr Leu Gly
 130 135 140

Gln Asn Ile Val Ser Leu Asn His Thr Arg Gln Ala Met Glu Ile Phe
 145 150 155 160

Lys Gly His Gly Asp His Asp Met Asn Leu Val Ser Thr Tyr Ile Thr
 165 170 175

Met Ala Gly Asn Tyr Thr Glu Met Gly Lys Tyr Thr Glu Ala Glu Glu
 180 185 190

Tyr Leu Thr Glu Ala Ile His Thr Val Arg Lys Ala Gly Asp Cys Phe
 195 200 205

Lys Glu Met Gln Leu Leu His Asn Phe Ala Leu Leu Tyr Ala Ala Met
 210 215 220

Asp Asn Ser Glu Lys Ser Ile Gln Phe Leu Glu Ile Val Leu Asp Asp
 225 230 235 240

Gln Ala Tyr Ala Ala Ser Asp Tyr Tyr Phe Asn Ala Val Phe Leu Met
 245 250 255

Ile Lys Glu Leu Phe Lys Val Gly Asp His Lys Arg Ala Ala Ala Phe
 260 265 270

Tyr Lys Glu Gly Lys Glu Arg Ser Lys Ser Ala Ala Asn Lys Ile Phe
 275 280 285

Asp Ala Lys Ile Asp Ile Leu Tyr Ala Ala Tyr Ala Gly Asp Gly Glu
 290 295 300

Gln Ala Val Lys Asp Cys Lys Asp Asn Ile Glu Ile Leu Phe Gln Thr
 305 310 315 320

Lys Gln Tyr Asp Ser Ala Arg Glu Leu Ser Leu Leu Thr Ala Asn Val
 325 330 335

Tyr Arg Ser Lys Ser Leu Tyr Lys Glu Ala Ala His Phe Phe Leu Glu
 340 345 350

Ala Ile Lys Ala Glu Glu Lys Met Lys Lys Val Glu Gly Met
 355 360 365

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<213> Bacillus licheniformis

<220>
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<222> (384)..(1433)

[illegible]

10295.204.ST25.txt

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 175 180 185
 gta gct gca gcg gga tat cat cac cat cca tat cct tat ccg ttc tat 989
 Val Ala Ala Ala Gly Tyr His His His Pro Tyr Pro Tyr Pro Phe Tyr
 190 195 200
 cct gga ggc tgc tgg att cct gtt tca ccg gtg ctg cct gga tcg gga 1037
 Pro Gly Gly Cys Trp Ile Pro Val Ser Pro Val Leu Pro Gly Ser Gly
 205 210 215
 ttg tgc cat cct tgg tat cca tat cct gct caa atg cct tat atg cat 1085
 Leu Cys His Pro Trp Tyr Pro Tyr Pro Ala Gln Met Pro Tyr Met His
 220 225 230
 cag cct agc tat gta tct cct gct gaa tat gac gat gat gac aac atg 1133
 Gln Pro Ser Tyr Val Ser Pro Ala Glu Tyr Asp Asp Asp Asp Asn Met
 235 240 245 250
 ggg cat gac aat gcc ggt cat cac gga tac cat cat cag ccg atg act 1181
 Gly His Asp Asn Ala Gly His His Gly Tyr His His Gln Pro Met Thr
 255 260 265
 gcc ccg gca tat gcg cct tac cag ccg ttc ccg gga ttt gca ccg cca 1229
 Ala Pro Ala Tyr Ala Pro Tyr Gln Pro Phe Pro Gly Phe Ala Pro Pro
 270 275 280
 aac gtc ggt cac gcc ggg gac cct aat atg gca cac ggc aaa gaa gat 1277
 Asn Val Gly His Ala Gly Asp Pro Asn Met Ala His Gly Lys Glu Asp
 285 290 295
 gac tgc ggg tgc ggg ccg ggc caa ttc ccg gga ggt ttt cca ggt gcg 1325
 Asp Cys Gly Cys Gly Pro Gly Gln Phe Pro Gly Gly Phe Pro Gly Ala
 300 305 310
 gcg cca tat gga cag atg ccg caa atg gga gct ccg tac ggt atg ggg 1373
 Ala Pro Tyr Gly Gln Met Pro Gln Met Gly Ala Pro Tyr Gly Met Gly
 315 320 325 330
 gga tac gga cag cag cct gca ggg gga cag atg ttt aac aga ccg gaa 1421
 Gly Tyr Gly Gln Gln Pro Ala Gly Gly Gln Met Phe Asn Arg Pro Glu
 335 340 345
 gat gat gaa gac tgattcggaa tgggacgatg atctatcggt ctttttttat 1473
 Asp Asp Glu Asp 350
 tgtggaccgc tataaacatt ttcattgctat ttaacgggaa tgtctataac tgtcaagggt 1533
 aactcttcgc atcccgacata tcctaaaaaa gagcgcaatg ctcaaattca gcggttttca 1593
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 ttacagaaat gcttgaaaac atgaacggga gacacggtgc aacaaacgta aacaatcgag 1833
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 atcacaaacca tttggtgaat acggcgggata caggctatga cag 1936

<210> 38
 <211> 350
 <212> PRT
 <213> Bacillus licheniformis

10295.204.ST25.txt

<400> 38

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Glu Arg Tyr Glu Val Asp Phe Glu Glu Leu Lys Lys Leu Asn Ser Gln
 20 25 30

Leu Ser Asn Pro Asp Leu Ile Met Pro Gly Met Lys Ile Lys Val Pro
 35 40 45

Ser Gly Gly Val Pro Val Lys Lys Glu Glu Gln Leu Asn Met Arg Lys
 50 55 60

Glu Leu Pro Lys Lys Gln Gln Glu His Pro Phe Ala Lys Glu Lys Pro
 65 70 75 80

Lys Ser Lys Leu Asp Val Glu Asp Ile Lys Pro Lys Glu Lys Pro Ser
 85 90 95

Val Pro Tyr Val Pro Pro Val Pro Asn Ile Gly Gln Ser Ser Leu Pro
 100 105 110

Glu Gly Asp Ile Ser Asn Leu Tyr Gln Ser Val Asn Gln Leu His Gln
 115 120 125

Pro Tyr Val Pro Pro Lys Pro Tyr Glu His Gln Glu Lys Gly Pro Asn
 130 135 140

Met Tyr Asn Pro Trp Thr Asn Glu Glu Glu Asn His Met Glu Asn Val
 145 150 155 160

Asn Tyr Pro Asn Val Pro Gln Pro Pro Asn Val Gly Ala Ala Gly Asp
 165 170 175

Glu Asn Lys Gln Phe His Gly Met Pro Asn Val Ala Ala Ala Gly Tyr
 180 185 190

His His His Pro Tyr Pro Tyr Pro Phe Tyr Pro Gly Gly Cys Trp Ile
 195 200 205

Pro Val Ser Pro Val Leu Pro Gly Ser Gly Leu Cys His Pro Trp Tyr
 210 215 220

Pro Tyr Pro Ala Gln Met Pro Tyr Met His Gln Pro Ser Tyr Val Ser
 225 230 235 240

Pro Ala Glu Tyr Asp Asp Asp Asp Asn Met Gly His Asp Asn Ala Gly
 245 250 255

His His Gly Tyr His His Gln Pro Met Thr Ala Pro Ala Tyr Ala Pro
 Page 51

10295.204.ST25.txt
265

260

270

Tyr Gln Pro Phe Pro Gly Phe Ala Pro Pro Asn Val Gly His Ala Gly
275 280 285

Asp Pro Asn Met Ala His Gly Lys Glu Asp Asp Cys Gly Cys Gly Pro
290 295 300

Gly Gln Phe Pro Gly Gly Phe Pro Gly Ala Ala Pro Tyr Gly Gln Met
305 310 315 320

Pro Gln Met Gly Ala Pro Tyr Gly Met Gly Gly Tyr Gly Gln Gln Pro
325 330 335

Ala Gly Gly Gln Met Phe Asn Arg Pro Glu Asp Asp Glu Asp
340 345 350

<210> 39
<211> 2027
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1526)

<400> 39
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ttgtttatct gaatgatccc ggctgcggcg gagataatac atgtgaccaa ttgttagaaa 180
gggggattct gatatgccta ggcagccatt caaactggga gatgaggtgt atgtcattta 240
ccggaatccg catgcagcga atgtggcgca tataaaggaa gctgaagtcg ttgatcatcc 300
gcttcacgaa ggcgaactgg cattgtttat gtatgataca tatcacgcct ttgccgaaga 360
tgatgccgtt ttttcttcat atgaagaggc ggaacggctt taccgtgaat tatttgacgg 420
gatatgaaga cattaccggt atatcacatc ctctaaatgc aaaaagtaat ggaaatatgc 480
aaaggatgtg tctgtttcca atg gta aaa ccg ttt gtt ccc caa ctc gtc tat 533
Met Val Lys Pro Phe Val Pro Gln Leu Val Tyr
1 5 10

att gaa ccg aga gcc ctg gaa tat ccg ctt gga aaa gag ctg agg gat 581
Ile Glu Pro Arg Ala Leu Glu Tyr Pro Leu Gly Lys Glu Leu Arg Asp
15 20 25

aaa ttt tca aac atg gga ctt gag atc agg gaa aca act tca cac aac 629
Lys Phe Ser Asn Met Gly Leu Glu Ile Arg Glu Thr Thr Ser His Asn
30 35 40

cag gtg agg aat atc ccg ggg gaa ggc cac ctg caa aaa tac aga aat 677
Gln Val Arg Asn Ile Pro Gly Glu Gly His Leu Gln Lys Tyr Arg Asn
45 50 55

gcg aaa tcc act ttg gtg atc ggc gtc aga aaa aca ttg aag ttc gat 725
Ala Lys Ser Thr Leu Val Ile Gly Val Arg Lys Thr Leu Lys Phe Asp
Page 52

10295.204.ST25.txt

60	65	70	75	
tcg tca aaa ccg tcc gca gaa tac gcg atc ccg ttt gca aca ggg tgt Ser Ser Lys Pro Ser Ala Glu Tyr Ala Ile Pro Phe Ala Thr Gly Cys 80 85 90				773
atg ggt cac tgt cat tac tgc tac ctg caa acg aca atg ggc agc aag Met Gly His Cys His Tyr Cys Tyr Leu Gln Thr Thr Met Gly Ser Lys 95 100 105				821
ccg tat atc aga acg tac gtc aat gtg gag gaa ata ctt gag cag gcg Pro Tyr Ile Arg Thr Tyr Val Asn Val Glu Glu Ile Leu Glu Gln Ala 110 115 120				869
gat caa tat ata aaa gaa agg gct ccc gaa gat acg cgg ttt gaa gct Asp Gln Tyr Ile Lys Glu Arg Ala Pro Glu Asp Thr Arg Phe Glu Ala 125 130 135				917
tcc tgc aca tcc gat atc gtc gga att gac cat ttg aca cat acg tta Ser Cys Thr Ser Asp Ile Val Gly Ile Asp His Leu Thr His Thr Leu 140 145 150 155				965
aaa cgc gcc att gag cat ttc ggt caa acc gac cat ggt aag ctg cgt Lys Arg Ala Ile Glu His Phe Gly Gln Thr Asp His Gly Lys Leu Arg 160 165 170				1013
ttc gtg aca aaa ttt cat cat gtc gac cat ttg ctc gat gcc aag cac Phe Val Thr Lys Phe His His Val Asp His Leu Leu Asp Ala Lys His 175 180 185				1061
aac gga aaa acg cgc ttc cgc ttc agc gtg aat gcc gaa tat gtc att Asn Gly Lys Thr Arg Phe Arg Phe Ser Val Asn Ala Glu Tyr Val Ile 190 195 200				1109
aaa agc ttt gaa ccc ggc aca tcc ccg ttg gat aaa cgg atc gaa gcc Lys Ser Phe Glu Pro Gly Thr Ser Pro Leu Asp Lys Arg Ile Glu Ala 205 210 215				1157
gcc gtg aaa gta gcg gaa gcg ggc tat ccg ctc ggt ttt atc atc gct Ala Val Lys Val Ala Glu Ala Gly Tyr Pro Leu Gly Phe Ile Ile Ala 220 225 230 235				1205
ccg att tat att cat gac ggc tgg cag gaa ggc tac aga gtt ctg ctg Pro Ile Tyr Ile His Asp Gly Trp Gln Glu Gly Tyr Arg Val Leu Leu 240 245 250				1253
gaa aag ctc gat cgt gcg ctg ccg cag cat gcg agg cgc gac atc acc Glu Lys Leu Asp Arg Ala Leu Pro Gln His Ala Arg Arg Asp Ile Thr 255 260 265				1301
ttt gaa atg atc cag cat aga ttc acg aag ccg gca aag aga gtc att Phe Glu Met Ile Gln His Arg Phe Thr Lys Pro Ala Lys Arg Val Ile 270 275 280				1349
gaa aaa aac tat cca aag aca aag ctc gaa ctg gat gaa gaa aaa cgg Glu Lys Asn Tyr Pro Lys Thr Lys Leu Glu Leu Asp Glu Glu Lys Arg 285 290 295				1397
cgc tat aaa tgg ggc aga tac ggg att ggc aaa tac att tat cag aag Arg Tyr Lys Trp Gly Arg Tyr Gly Ile Gly Lys Tyr Ile Tyr Gln Lys 300 305 310 315				1445
gat gaa gaa gca gag ctt cgc agc gcc ctt gaa tcg tat atc gac aac Asp Glu Glu Ala Glu Leu Arg Ser Ala Leu Glu Ser Tyr Ile Asp Asn 320 325 330				1493
tat ttt ccc gaa gca aaa atc gaa tat ttc aca taacagagct ttagttgata Tyr Phe Pro Glu Ala Lys Ile Glu Tyr Phe Thr				1546

10295.204.ST25.txt
340

335

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aagctctgtt ttttgtttg aaaacattat gttaaaaaag gatttttcca ctccattaac 1606
accgcataat caagcgattc ctcatcttca atgtagccgg gaatcacaca aactggagag 1666
cgtccgcaat gaagcaggaa cgagagcact ggatcgcgct tttccccgtc caatacagct 1726
tgaacatact gttcgggctt catttcttca gccgacttgt gataatgggg aatccgtccg 1786
ccgccaatga gacgcttgag cccttttaaag accgtcagtt catacatgga ttgcatcagc 1846
cgcattccga tgccgagttt tcgatagtcg ggggacacgg aaatatcgac gacataaagg 1906
gagtttccat cgttttgatg tgtgccgata taccggttgt ccgtcacttc atcccagctg 1966
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c 2027

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<210> 40
 <211> 342
 <212> PRT
 <213> Bacillus licheniformis

<400> 40

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20 25 30

Gly Leu Glu Ile Arg Glu Thr Thr Ser His Asn Gln Val Arg Asn Ile
35 40 45

Pro Gly Glu Gly His Leu Gln Lys Tyr Arg Asn Ala Lys Ser Thr Leu
50 55 60

Val Ile Gly Val Arg Lys Thr Leu Lys Phe Asp Ser Ser Lys Pro Ser
65 70 75 80

Ala Glu Tyr Ala Ile Pro Phe Ala Thr Gly Cys Met Gly His Cys His
85 90 95

Tyr Cys Tyr Leu Gln Thr Thr Met Gly Ser Lys Pro Tyr Ile Arg Thr
100 105 110

Tyr Val Asn Val Glu Glu Ile Leu Glu Gln Ala Asp Gln Tyr Ile Lys
115 120 125

Glu Arg Ala Pro Glu Asp Thr Arg Phe Glu Ala Ser Cys Thr Ser Asp
130 135 140

Ile Val Gly Ile Asp His Leu Thr His Thr Leu Lys Arg Ala Ile Glu
145 150 155 160

10295.204.ST25.txt

His Phe Gly Gln Thr Asp His Gly Lys Leu Arg Phe Val Thr Lys Phe
 165 170 175

His His Val Asp His Leu Leu Asp Ala Lys His Asn Gly Lys Thr Arg
 180 185 190

Phe Arg Phe Ser Val Asn Ala Glu Tyr Val Ile Lys Ser Phe Glu Pro
 195 200 205

Gly Thr Ser Pro Leu Asp Lys Arg Ile Glu Ala Ala Val Lys Val Ala
 210 215 220

Glu Ala Gly Tyr Pro Leu Gly Phe Ile Ile Ala Pro Ile Tyr Ile His
 225 230 235 240

Asp Gly Trp Gln Glu Gly Tyr Arg Val Leu Leu Glu Lys Leu Asp Arg
 245 250 255

Ala Leu Pro Gln His Ala Arg Arg Asp Ile Thr Phe Glu Met Ile Gln
 260 265 270

His Arg Phe Thr Lys Pro Ala Lys Arg Val Ile Glu Lys Asn Tyr Pro
 275 280 285

Lys Thr Lys Leu Glu Leu Asp Glu Glu Lys Arg Arg Tyr Lys Trp Gly
 290 295 300

Arg Tyr Gly Ile Gly Lys Tyr Ile Tyr Gln Lys Asp Glu Glu Ala Glu
 305 310 315 320

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 325 330 335

Lys Ile Glu Tyr Phe Thr
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 <213> Bacillus licheniformis

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 <222> (501)..(905)

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 tggaatgatc atatgaacat gttcaactat gtattcggcc agtacaaaac atatatcatc 180
 gccaaaaaag gcgagattcc gaaattaaaa gactcttttt acggacatac agcttttatt 240
 aaacgggatg tcacatatct tttaaacgaa gaggaaaaag aagatgtgaa gggtgatatc 300

gagcttcttg	aaccgaaaaa	atcatggcgt	aaaaacaaaa	aagaaatccc	ggacatcatc		360
ggagaaatga	acgtcatgtt	cgacggaaaa	acgattgcaa	gcgtaccgat	ctattatgaa		420
aacgagcgaa	acaaaaatcc	gaaaaaatcg	tttttcgaga	cctttcaatc	cgtattccaa		480
aaagcggcgg	gcgggttcac	atg gtc aat ata atc tgg gtc ggc tta acg gtg					533
		Met Val Asn Ile Ile Trp Val Gly Leu Thr Val					
		1		5		10	
atc ggt atg gtg ttt gcg ctt ttc aac ggc acg gtt cag gaa gtt aat							581
Ile Gly Met Val Phe Ala Leu Phe Asn Gly Thr Val Gln Glu Val Asn							
gaa gct gta ttt aaa gga tcg aag gaa gcc gtc acg att gtg atc gga							629
Glu Ala Val Phe Lys Gly Ser Lys Glu Ala Val Thr Ile Val Ile Gly							
ctg atg agc gtc ctt gtt ttt tgg ctg ggg gtg atg aaa atc gct gaa							677
Leu Met Ser Val Leu Val Phe Trp Leu Gly Val Met Lys Ile Ala Glu							
cag tcc ggg ctt ctc gaa aaa ttc agc agg ctg tgc cgg ccg ttc att							725
Gln Ser Gly Leu Leu Glu Lys Phe Ser Arg Leu Cys Arg Pro Phe Ile							
tcg aag ctg ttt ccc gag atc cct ccg gat cat ccg gcg atg gga tat							773
Ser Lys Leu Phe Pro Glu Ile Pro Pro Asp His Pro Ala Met Gly Tyr							
att tta tcc aat tta atg gcc aac ttt ttc gga ttg ggc aat gca gcg							821
Ile Leu Ser Asn Leu Met Ala Asn Phe Phe Gly Leu Gly Asn Ala Ala							
aca ccg ctc ggt att aaa gcg atg gaa cag atg aag gcg ctc aac ccg							869
Thr Pro Leu Gly Ile Lys Ala Met Glu Gln Met Lys Ala Leu Asn Arg							
aac cgc agg gaa gcg agc cgc tca atg cac cca ggc							905
Asn Arg Arg Glu Ala Ser Arg Ser Met His Pro Gly							

<210>	42
<211>	135
<212>	PRT
<213>	Bacillus licheniformis

<400> 42

Met Val Asn Ile Ile Trp Val Gly Leu Thr Val Ile Gly Met Val Phe
1 5 10 15

Ala Leu Phe Asn Gly Thr Val Gln Glu Val Asn Glu Ala Val Phe Lys
20 25 30

Gly Ser Lys Glu Ala Val Thr Ile Val Ile Gly Leu Met Ser Val Leu
35 40 45

Val Phe Trp Leu Gly Val Met Lys Ile Ala Glu Gln Ser Gly Leu Leu
50 55 60

Glu Lys Phe Ser Arg Leu Cys Arg Pro Phe Ile Ser Lys Leu Phe Pro

10295.204.ST25.txt

65

70

75

80

Glu Ile Pro Pro Asp His Pro Ala Met Gly Tyr Ile Leu Ser Asn Leu
85 90 95

Met Ala Asn Phe Phe Gly Leu Gly Asn Ala Ala Thr Pro Leu Gly Ile
100 105 110

Lys Ala Met Glu Gln Met Lys Ala Leu Asn Arg Asn Arg Arg Glu Ala
115 120 125

Ser Arg Ser Met His Pro Gly
130 135

<210> 43
<211> 1568
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1076)

<220>
<221> CDS
<222> (1112)..(1567)

<400> 43
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caatccttta tcgtcagcgc ggaacaaaaa tctatccaag tgaaaacgtt gggcgcggcc 180
gatattacac tctatttgca aaagtgcagc gaactgttaa attcgaacct ttcggccgta 240
ccccaaaaa agtgagcgta tctcctgtag cctaaccttt aaacgaaact ccggtcgttc 300
tgaccggagt tttttacatt cagcaccatg acttgcttaa aacaccttcc cgacgcctaa 360
ataaggccgg gtttccgctc tgattctgct tcgttaaagt atataaacgt gtttcattta 420
tactgccttc tctgttataa ttcaaagtac aaactgaatc agactcctaa aagagagacc 480
aaacgattgg gagtgccaaa atg gaa gaa act tcg aaa aaa cga gaa aag aat 533
Met Glu Glu Thr Ser Lys Lys Arg Glu Lys Asn 10

atg gac gat aag gct ttg acc cat gag ctt atc cat ctg ctc agc cac 581
Met Asp Asp Lys Ala Leu Thr His Glu Leu Ile His Leu Leu Ser His 25

tca agg cac gac tgg atg aat aaa ctg caa ttg att aaa gga aac tta 629
Ser Arg His Asp Trp Met Asn Lys Leu Gln Leu Ile Lys Gly Asn Leu 40

aca tta aaa aag tat gac cgc gta ttt gaa att atc gat gaa gtg gtc 677
Thr Leu Lys Lys Tyr Asp Arg Val Phe Glu Ile Ile Asp Glu Val Val 55

atc gaa gct cag cat gaa tca aag ctt tca aac ctt aga atc ccg cgc 725
Ile Glu Ala Gln His Glu Ser Lys Leu Ser Asn Leu Arg Ile Pro Arg

10295.204.ST25.txt

60	65	70	75	
gcg gcg tat gag ctg ctt aca ttt aac tgg atg gcc cat tcg ctg acg Ala Ala Tyr Glu Leu Leu Thr Phe Asn Trp Met Ala His Ser Leu Thr	80	85	90	773
ctt gaa tat gag gtg atc ggt caa gtc aag gat ttg tca gct tat gaa Leu Glu Tyr Glu Val Ile Gly Gln Val Lys Asp Leu Ser Ala Tyr Glu	95	100	105	821
gaa agg ctc gtc gtt ctc atc aga aag ctg ttt ggg att ttt gac gat Glu Arg Leu Val Val Leu Ile Arg Lys Leu Phe Gly Ile Phe Asp Asp	110	115	120	869
gcc gtt ttg aaa ggc agc gac aat cat ctg acg atc acg ctg cag acg Ala Val Leu Lys Gly Ser Asp Asn His Leu Thr Ile Thr Leu Gln Thr	125	130	135	917
gac ggt ccg gac gac cgc ctc gtc atc ttt ctc gat ttc cac ggc gta Asp Gly Pro Asp Asp Arg Leu Val Ile Phe Leu Asp Phe His Gly Val	140	145	150	965
ttc aca aag ctg acc ggt atc aaa gac ttt cat cat tca ctg gcc gac Phe Thr Lys Leu Thr Gly Ile Lys Asp Phe His His Ser Leu Ala Asp	160	165	170	1013
ttt tat gaa atc aag cgg ttt gat gta aca gac cgt gag tgc atc gcc Phe Tyr Glu Ile Lys Arg Phe Asp Val Thr Asp Arg Glu Cys Ile Ala	175	180	185	1061
gaa att cat atc aag taaagcgggt ttttaggaat agaacggagg acatt atg Glu Ile His Ile Lys Met	190			1114
ttt gtt gat cag gtg aaa ata tac gta aaa ggc gga gac gga ggc aac Phe Val Asp Gln Val Lys Ile Tyr Val Lys Gly Gly Asp Gly Gly Asn	195	200	205	1162
ggt atg gtt gct ttc cgc cgc gaa aaa tat gtg cca aaa gga ggc cct Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Lys Gly Gly Pro	210	215	220	1210
gcc gga ggt gac ggc gga aaa ggc gga gac gtc gtt ttc aaa gtt gac Ala Gly Gly Asp Gly Gly Lys Gly Gly Val Val Phe Lys Val Asp	230	235	240	1258
gaa ggt ctc agc acg ctg atg gat ttt aga tat caa aga cat ttt aag Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe Lys	245	250	255	1306
gca gcg cgc gga gaa cac ggc atg tct aaa aac cag cac ggc cga aat Ala Ala Arg Gly Glu His Gly Met Ser Lys Asn Gln His Gly Arg Asn	260	265	270	1354
gcc gaa gac atg gtt gtg aaa gtc ccg ccc ggc acg gtt gtc att gac Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile Asp	275	280	285	1402
gat gat aca aaa cag gtc atc gct gat tta acg gag cac gga cag gaa Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln Glu	290	295	300	1450
gcc gtc atc gca aaa ggg gga cgc ggc gga cgg ggc aat aca cgt ttt Ala Val Ile Ala Lys Gly Gly Arg Gly Gly Arg Gly Asn Thr Arg Phe	310	315	320	1498
gcg acg cct gcc aac ccg gcg ccg cag ctt tct gaa aac ggc gaa ccc Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu Pro				1546

10295.204.ST25.txt
330

325

335

1568

ggc aag gag cgc tat att gtt c
Gly Lys Glu Arg Tyr Ile Val
340

<210> 44
<211> 192
<212> PRT
<213> Bacillus licheniformis

<400> 44

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20 25 30

Met Asn Lys Leu Gln Leu Ile Lys Gly Asn Leu Thr Leu Lys Lys Tyr
35 40 45

Asp Arg Val Phe Glu Ile Ile Asp Glu Val Val Ile Glu Ala Gln His
50 55 60

Glu Ser Lys Leu Ser Asn Leu Arg Ile Pro Arg Ala Ala Tyr Glu Leu
65 70 75 80

Leu Thr Phe Asn Trp Met Ala His Ser Leu Thr Leu Glu Tyr Glu Val
85 90 95

Ile Gly Gln Val Lys Asp Leu Ser Ala Tyr Glu Glu Arg Leu Val Val
100 105 110

Leu Ile Arg Lys Leu Phe Gly Ile Phe Asp Asp Ala Val Leu Lys Gly
115 120 125

Ser Asp Asn His Leu Thr Ile Thr Leu Gln Thr Asp Gly Pro Asp Asp
130 135 140

Arg Leu Val Ile Phe Leu Asp Phe His Gly Val Phe Thr Lys Leu Thr
145 150 155 160

Gly Ile Lys Asp Phe His His Ser Leu Ala Asp Phe Tyr Glu Ile Lys
165 170 175

Arg Phe Asp Val Thr Asp Arg Glu Cys Ile Ala Glu Ile His Ile Lys
180 185 190

<210> 45
<211> 152
<212> PRT
<213> Bacillus licheniformis

<400> 45

10295.204.ST25.txt

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Pro Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp Val Val Phe Lys Val
 35 40 45

Asp Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe
 50 55 60

Lys Ala Ala Arg Gly Glu His Gly Met Ser Lys Asn Gln His Gly Arg
 65 70 75 80

Asn Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile
 85 90 95

Asp Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln
 100 105 110

Glu Ala Val Ile Ala Lys Gly Gly Arg Gly Gly Arg Gly Asn Thr Arg
 115 120 125

Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu
 130 135 140

Pro Gly Lys Glu Arg Tyr Ile Val
 145 150

<210> 46
 <211> 1849
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 <222> (501)..(1346)

<400> 46
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 agtccggctg aaaagggctt tggaatcggg caaacaaaac tatgatttca tgattattga 120
 ctgcccgcg tcattagggc tgcttacaat caatgcgctt acggcttccg attccgctcg 180
 gattccggtc cagtgcgagt attatgcgct ggaagggctg agccagctgc tcaactctgt 240
 ccggctcgtg caaaaacatt taaatacgga tctgatgatc gacggcgat tgcgtgacaat 300
 gcttgatgca agaacgaatt taggcataca ggtcatcgaa gaagtga aaa agtacttccg 360
 cgataaagta taaaaaacgg ttatcccccg gaatgtccgg ctccagtgaag cgccgagtca 420
 tggaaagccg atcattttat atgatccccg ttccagagga gcggaagtct atttagaatt 480

10295.204.ST25.txt

agcaaaggaa gtggctgcga atg cct aaa ggt ctc gga aaa ggg att aat gca 533
 Met Pro Lys Gly Leu Gly Lys Gly Ile Asn Ala
 1 5 10

ttg ttt tca aat gtt gat tta tcc gaa gaa acg gtt gag gaa atc aag 581
 Leu Phe Ser Asn Val Asp Leu Ser Glu Glu Thr Val Glu Glu Ile Lys
 15 20 25

ctg caa gac ttg cgg ccc aac cct tat cag cca aga aaa acg ttt gat 629
 Leu Gln Asp Leu Arg Pro Asn Pro Tyr Gln Pro Arg Lys Thr Phe Asp
 30 35 40

gac caa tcg tta aaa gat ttg aag gag tcc att ttg cag cac ggt gtt 677
 Asp Gln Ser Leu Lys Asp Leu Lys Glu Ser Ile Leu Gln His Gly Val
 45 50 55

ttg cag ccc atc atc gtc aga aag tca att aaa ggc tat gac att gtg 725
 Leu Gln Pro Ile Ile Val Arg Lys Ser Ile Lys Gly Tyr Asp Ile Val
 60 65 70 75

gcc gga gaa cgc cgt ttc cgg gct gct gaa aag gcc gga ttg gaa acc 773
 Ala Gly Glu Arg Arg Phe Arg Ala Ala Glu Lys Ala Gly Leu Glu Thr
 80 85 90

att cct gcg att gtg cgc gag ctg tcg gaa tcc ctg atg atg gag att 821
 Ile Pro Ala Ile Val Arg Glu Leu Ser Glu Ser Leu Met Met Glu Ile
 95 100 105

gcc cta ttg gaa aat ctt caa cga gaa gac ctg tct ccg ctt gaa gaa 869
 Ala Leu Leu Glu Asn Leu Gln Arg Glu Asp Leu Ser Pro Leu Glu Glu
 110 115 120

gca aaa gcc tat gaa tct ttg ctc aaa cat ctc gat atg acc cag gaa 917
 Ala Lys Ala Tyr Glu Ser Leu Leu Lys His Leu Asp Met Thr Gln Glu
 125 130 135

cag ctg gcg aaa agg ctt gga aaa agc agg cct cac atc gcc aac cac 965
 Gln Leu Ala Lys Arg Leu Gly Lys Ser Arg Pro His Ile Ala Asn His
 140 145 150 155

ttg cgg ctg ctg aca ctt cct gaa gac gtt caa aag tta atc gac aac 1013
 Leu Arg Leu Leu Thr Leu Pro Glu Asp Val Gln Lys Leu Ile Asp Asn
 160 165 170

ggc acg tta tcg atg ggc cat ggc cga aca ttg ctt gga ttg aaa aac 1061
 Gly Thr Leu Ser Met Gly His Gly Arg Thr Leu Leu Gly Leu Lys Asn
 175 180 185

aag aaa aag ctt gag ccg ctt gtt caa aag gtc gtg tcc gaa cag ttg 1109
 Lys Lys Lys Leu Glu Pro Leu Val Gln Lys Val Val Ser Glu Gln Leu
 190 195 200

aac gtc cgc cag ttg gaa aag tta att caa cag ttg aac gct gat gtt 1157
 Asn Val Arg Gln Leu Glu Lys Leu Ile Gln Gln Leu Asn Ala Asp Val
 205 210 215

cca cgt gaa aca aag aag ccg aaa caa gtc aaa gat gca gtg atc aag 1205
 Pro Arg Glu Thr Lys Lys Pro Lys Gln Val Lys Asp Ala Val Ile Lys
 220 225 230 235

gaa cgg gaa tcg tat ttg cga aac tat ttt gga aca ccg gtg acc att 1253
 Glu Arg Glu Ser Tyr Leu Arg Asn Tyr Phe Gly Thr Pro Val Thr Ile
 240 245 250

aaa aag caa aag aaa aaa ggc agg atc gaa atc gaa ttc tac tca aat 1301
 Lys Lys Gln Lys Lys Lys Gly Arg Ile Glu Ile Glu Phe Tyr Ser Asn
 255 260 265

10295.204.ST25.txt

gaa gac ttg gag cgt att ctc gaa tta ttg gct caa gaa gac gca 1346
 Glu Asp Leu Glu Arg Ile Leu Glu Leu Leu Ala Gln Glu Asp Ala
 270 275 280
 taagcttaaa aaccatctga tcatgtacag atggtttttt tatgacattc ttccggtcat 1406
 tctttcaatt ggtgacacat ggcgccgctg cgatccggtc ttttccagat gcgacagccc 1466
 gtccgcaagc acatttgcca tgctcatgac aagattgagc cttgtatttt gcaggacaaa 1526
 atactccata aaaccgctga cattgacaat tccgttaata tgcacgtggc cgacttccgg 1586
 caaacttttc tgaacgcctg ctcccggctt caaaggccct ttgccgattt ggaaagaccc 1646
 cacgcttttg gttcgtccaa gacaggcgctc gatcgcgatc ataaaaggat tttgatgctg 1706
 ctgatgaata tgatcaagct tttcatttaa gttcacggcg tgaaccgggt cggcaagcgt 1766
 tccatagaca tgaaaacgtg tcagctgctt tgcggagagt ttcattccta cgaggggacc 1826
 gagcgaatct ccggtcgcgc ggt 1849

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 <211> 282
 <212> PRT
 <213> Bacillus licheniformis

<400> 47

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1 5 10 15

Asp Leu Ser Glu Glu Thr Val Glu Glu Ile Lys Leu Gln Asp Leu Arg
20 25 30

Pro Asn Pro Tyr Gln Pro Arg Lys Thr Phe Asp Asp Gln Ser Leu Lys
35 40 45

Asp Leu Lys Glu Ser Ile Leu Gln His Gly Val Leu Gln Pro Ile Ile
50 55 60

Val Arg Lys Ser Ile Lys Gly Tyr Asp Ile Val Ala Gly Glu Arg Arg
65 70 75 80

Phe Arg Ala Ala Glu Lys Ala Gly Leu Glu Thr Ile Pro Ala Ile Val
85 90 95

Arg Glu Leu Ser Glu Ser Leu Met Met Glu Ile Ala Leu Leu Glu Asn
100 105 110

Leu Gln Arg Glu Asp Leu Ser Pro Leu Glu Glu Ala Lys Ala Tyr Glu
115 120 125

Ser Leu Leu Lys His Leu Asp Met Thr Gln Glu Gln Leu Ala Lys Arg
130 135 140

Leu Gly Lys Ser Arg Pro His Ile Ala Asn His Leu Arg Leu Leu Thr
145 150 155 160

10295.204.ST25.txt

Leu Pro Glu Asp Val Gln Lys Leu Ile Asp Asn Gly Thr Leu Ser Met
 165 170 175

Gly His Gly Arg Thr Leu Leu Gly Leu Lys Asn Lys Lys Lys Leu Glu
 180 185 190

Pro Leu Val Gln Lys Val Val Ser Glu Gln Leu Asn Val Arg Gln Leu
 195 200 205

Glu Lys Leu Ile Gln Gln Leu Asn Ala Asp Val Pro Arg Glu Thr Lys
 210 215 220

Lys Pro Lys Gln Val Lys Asp Ala Val Ile Lys Glu Arg Glu Ser Tyr
 225 230 235 240

Leu Arg Asn Tyr Phe Gly Thr Pro Val Thr Ile Lys Lys Gln Lys Lys
 245 250 255

Lys Gly Arg Ile Glu Ile Glu Phe Tyr Ser Asn Glu Asp Leu Glu Arg
 260 265 270

Ile Leu Glu Leu Leu Ala Gln Glu Asp Ala
 275 280

<210> 48
 <211> 3490
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 <222> (501)..(2987)

<400> 48
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 tattaaaatt tctattgacg gatagggcaa tcctttgtaa tatagaactt gtgcgtttaa 120
 agaaatcaac aacatggcgg tgtagctcag ctggctagag cgtacgggtc ataccctga 180
 ggtcgggggt tcgatcccct ccgccgctac ttatatgaag gcccgttggt caagtggtta 240
 agacaccgcc ctttcacggc ggtaacacgg gttcgaatcc cgtacgggtc attccggaaa 300
 ccggcttctt ctgaagccgg ttttttgctg cataaaaata tgcaaaataa cgggaatgga 360
 ctcgacttat caagagtgat tgaagcatgc tacaaaaagc gtcgaacagt tctttgaatt 420
 cgttaccttc ttttgacaaa atcctatttc atctttcgct ataatggcaa gcaacgaata 480
 aacgagtggg agatgagagc atg gaa aaa gcg gaa aga aga gtg aac agc cca 533
 Met Glu Lys Ala Glu Arg Arg Val Asn Ser Pro
 1 5 10
 ata gct gga cct gct gtt caa aaa ttg tat tca tgg ttt ggc agc atg 581
 Ile Ala Gly Pro Ala Val Gln Lys Leu Tyr Ser Trp Phe Gly Ser Met
 15 20 25

10295.204.ST25.txt

acg aag ctt atg atg cag cat tta tat tcc ctc ttt ttt tat aaa ggg 629
 Thr Lys Leu Met Met Gln His Leu Tyr Ser Leu Phe Tyr Lys Gly
 30 35 40

ctg atc tat atg gtc atc ggt ttt tta ttg gga cga gcc ttc att ctg 677
 Leu Ile Tyr Met Val Ile Gly Phe Leu Leu Gly Arg Ala Phe Ile Leu
 45 50 55

tca gag gtc att ccc ttt gct ctt cca ttt ttc gga gcg atg ctt tta 725
 Ser Glu Val Ile Pro Phe Ala Leu Pro Phe Phe Gly Ala Met Leu Leu
 60 65 70 75

atc aaa aaa gat aaa gct ttc ctt gca tgc ctg gcg ctt ctt gcc gga 773
 Ile Lys Lys Asp Lys Ala Phe Leu Ala Cys Leu Ala Leu Leu Ala Gly
 80 85 90

gct ctg agc ata tcg cct cag cat tcg ctg ttc gtg ctt gcg gct ctg 821
 Ala Leu Ser Ile Ser Pro Gln His Ser Leu Phe Val Leu Ala Ala Leu
 95 100 105

ttt gca ttt gcg ata tgt tca aaa atg acg tcc ctt att ata aaa gac 869
 Phe Ala Phe Ala Ile Cys Ser Lys Met Thr Ser Leu Ile Ile Lys Asp
 110 115 120

cgt gtc aga acg ctg cct gtc gtc gtc ttt ttg gcg atg gct gtg aca 917
 Arg Val Arg Thr Leu Pro Val Val Val Phe Leu Ala Met Ala Val Thr
 125 130 135

aga tgc gga ttc gta tat gcc gaa tac gga acg gtt tca ggt tat cac 965
 Arg Cys Gly Phe Val Tyr Ala Glu Tyr Gly Thr Val Ser Gly Tyr His
 140 145 150 155

tat att atg gct ttc gtt gaa gcc gga tta tcg ttt atc ctc aca ttg 1013
 Tyr Ile Met Ala Phe Val Glu Ala Gly Leu Ser Phe Ile Leu Thr Leu
 160 165 170

att ttt ctg caa agc ctg ccg att gtc aca tca aag cgg gcg aaa cag 1061
 Ile Phe Leu Gln Ser Leu Pro Ile Val Thr Ser Lys Arg Ala Lys Gln
 175 180 185

tcg ctg aaa att gaa gag atc att tgt ttt atg att tta atc gct tcc 1109
 Ser Leu Lys Ile Glu Glu Ile Ile Cys Phe Met Ile Leu Ile Ala Ser
 190 195 200

gtt ctc acg ggc ttg aca ggc gtt tca ttt caa ggc atg cag gct gaa 1157
 Val Leu Thr Gly Leu Thr Gly Val Ser Phe Gln Gly Met Gln Ala Glu
 205 210 215

ctg ata ttg gcc cgt tat gtc gtg ctc gct ttc gcg ttc atc gga ggc 1205
 Leu Ile Leu Ala Arg Tyr Val Val Leu Ala Phe Ala Phe Ile Gly Gly
 220 225 230 235

gca agc atc ggc tgt aca gtc ggg gtt gtg acc ggg ctg att ctc agc 1253
 Ala Ser Ile Gly Cys Thr Val Gly Val Val Thr Gly Leu Ile Leu Ser
 240 245 250

ctc tca aac atc ggc aat tta tat cag atg agc ctg ctg gct ttc tca 1301
 Leu Ser Asn Ile Gly Asn Leu Tyr Gln Met Ser Leu Leu Ala Phe Ser
 255 260 265

ggc ctt ctc ggc ggt ttg cta aaa gaa gga aaa aag ttc ggc gca gcg 1349
 Gly Leu Leu Gly Gly Leu Leu Lys Glu Gly Lys Lys Phe Gly Ala Ala
 270 275 280

gtc ggc tta ttg att gga tct cta ttg att tct ctg tac gga gaa ggt 1397
 Val Gly Leu Leu Ile Gly Ser Leu Leu Ile Ser Leu Tyr Gly Glu Gly
 285 290 295

10295.204.ST25.txt

tcg gct gaa tta gtg ccg acg ctt tat gaa tct ctg att gca atc ggc Ser Ala Glu Leu Val Pro Thr Leu Tyr Glu Ser Leu Ile Ala Ile Gly 300 305 310 315	1445
ctg ttc ctt tta acc cct cag tcg att acg aaa aaa gtg gcc aag tat Leu Phe Leu Leu Thr Pro Gln Ser Ile Thr Lys Lys Val Ala Lys Tyr 320 325 330	1493
ata cct gga acg act gag cac gcc cag gaa cag cag cag tat gca agg Ile Pro Gly Thr Thr Glu His Ala Gln Glu Gln Gln Tyr Ala Arg 335 340 345	1541
aaa atc cgc gat gtc acc gcc caa aaa gtc gat cag ttt tcg aac gtt Lys Ile Arg Asp Val Thr Ala Gln Lys Val Asp Gln Phe Ser Asn Val 350 355 360	1589
ttt cac gct tta tcc gaa agc ttc gct acc ttt tat cat tca gct ccg Phe His Ala Leu Ser Glu Ser Phe Ala Thr Phe Tyr His Ser Ala Pro 365 370 375	1637
gac gat gaa gga aaa gaa aaa gag atc gat ctg ttt ttg agc acg gtg Asp Asp Glu Gly Lys Glu Lys Glu Ile Asp Leu Phe Leu Ser Thr Val 380 385 390 395	1685
aca gaa cat tcc tgt cag tca tgc tat aag aaa aac aag tgc tgg gtt Thr Glu His Ser Cys Gln Ser Cys Tyr Lys Lys Asn Lys Cys Trp Val 400 405 410	1733
cag aac ttt gat aaa aca tat gat ttg atg aaa cgg gtt atg cag gaa Gln Asn Phe Asp Lys Thr Tyr Asp Leu Met Lys Arg Val Met Gln Glu 415 420 425	1781
acg gaa gaa aag caa tat ttt aaa aac cgc aag ctg aaa aag gag ttt Thr Glu Glu Lys Gln Tyr Phe Lys Asn Arg Lys Leu Lys Lys Glu Phe 430 435 440	1829
cat cag cac tgc tcc aaa tca aag caa gta gaa gcg ctg att gaa gac His Gln His Cys Ser Lys Ser Lys Gln Val Glu Ala Leu Ile Glu Asp 445 450 455	1877
gag ctg act cat ttt agg gcg aac cag aca tta aaa caa aag gtg cat Glu Leu Thr His Phe Arg Ala Asn Gln Thr Leu Lys Gln Lys Val His 460 465 470 475	1925
gac agc aga cgt ctc gtt gca gag cag ctt ctc gcc gtt tct cag gtt Asp Ser Arg Arg Leu Val Ala Glu Gln Leu Leu Gly Val Ser Gln Val 480 485 490	1973
atg gcg gac ttt tct cgg gaa ata aaa agg gaa agg gag cag cat ttt Met Ala Asp Phe Ser Arg Glu Ile Lys Arg Glu Arg Glu Gln His Phe 495 500 505	2021
att caa gaa gag caa att cgg gat gcg ctg cag cac ttc ggc atc gag Ile Gln Glu Glu Gln Ile Arg Asp Ala Leu Gln His Phe Gly Ile Glu 510 515 520	2069
att cag caa gtc gaa ata tac agc ctt gag cag gga aac atc gat att Ile Gln Gln Val Glu Ile Tyr Ser Leu Glu Gln Gly Asn Ile Asp Ile 525 530 535	2117
gaa atg agt atc ccg tat tgc aac gcc cat gga gag tgt gaa aaa atc Glu Met Ser Ile Pro Tyr Cys Asn Gly His Gly Glu Cys Glu Lys Ile 540 545 550 555	2165
atc gct ccg atg ctg tcc gat att ttg gaa gaa caa att atc gtc aaa Ile Ala Pro Met Leu Ser Asp Ile Leu Glu Glu Gln Ile Ile Val Lys 560 565 570	2213

10295.204.ST25.txt

gca gaa cag tgc gcc ggc cat ccg aat gga tat tgt cat gtt gcc ttc 2261
 Ala Glu Gln Cys Ala Gly His Pro Asn Gly Tyr Cys His Val Ala Phe
 575 580 585

ggt tcg gcg aag tca tac agg gtg gtg aca gga gcc gcg cat gca gca 2309
 Gly Ser Ala Lys Ser Tyr Arg Val Val Thr Gly Ala Ala His Ala Ala
 590 595 600

aaa ggc gga ggg ctt gtc tcc ggc gac agc tac aat atg atg gag ctc 2357
 Lys Gly Gly Gly Leu Val Ser Gly Asp Ser Tyr Asn Met Met Glu Leu
 605 610 615

ggc acc ggc aaa tat gcc gcc gcc att agc gat ggt atg gga aat ggc 2405
 Gly Thr Gly Lys Tyr Ala Ala Ala Ile Ser Asp Gly Met Gly Asn Gly
 620 625 630 635

gca agg gcc cat ttt gaa agc aat gag acg atc aag ctg ctg gaa aag 2453
 Ala Arg Ala His Phe Glu Ser Asn Glu Thr Ile Lys Leu Leu Glu Lys
 640 645 650

att ctt cag tcg ggc atc gac gaa aaa gtg gcg att aaa acg att aac 2501
 Ile Leu Gln Ser Gly Ile Asp Glu Lys Val Ala Ile Lys Thr Ile Asn
 655 660 665

agc att ctt tca tta agg aca aca gat gaa att tat tcg aca ttg gat 2549
 Ser Ile Leu Ser Leu Arg Thr Thr Asp Glu Ile Tyr Ser Thr Leu Asp
 670 675 680

tta tcg gtc atc gat ctt cag gat gcg agc tgc aag ttt ttg aaa atc 2597
 Leu Ser Val Ile Asp Leu Gln Asp Ala Ser Cys Lys Phe Leu Lys Ile
 685 690 695

ggc tcc acc ccg agc ttt att aaa aga ggc gat caa att ata aaa gtg 2645
 Gly Ser Thr Pro Ser Phe Ile Lys Arg Gly Asp Gln Ile Ile Lys Val
 700 705 710 715

cag gcc agc aat ctg ccg atc ggc atc att aca gaa ttc gat gtc gat 2693
 Gln Ala Ser Asn Leu Pro Ile Gly Ile Ile Thr Glu Phe Asp Val Asp
 720 725 730

gtt gtc agc gag caa tta aaa gcg gga gac ctt ttg atc atg atg agc 2741
 Val Val Ser Glu Gln Leu Lys Ala Gly Asp Leu Leu Ile Met Met Ser
 735 740 745

gac gga atc ttt gaa ggg ccg aga cat gtg gaa aat cat gat ctg tgg 2789
 Asp Gly Ile Phe Glu Gly Pro Arg His Val Glu Asn His Asp Leu Trp
 750 755 760

atg aag cgc aaa ttg aaa tcg ctg aaa acc gag gag ccg cag gaa atc 2837
 Met Lys Arg Lys Leu Lys Ser Leu Lys Thr Glu Glu Pro Gln Glu Ile
 765 770 775

gcc gac tta atc atg gaa gaa gtg atc cgg aca agg tcg ggt ctg att 2885
 Ala Asp Leu Ile Met Glu Glu Val Ile Arg Thr Arg Ser Gly Leu Ile
 780 785 790 795

gag gac gac atg acg gtg att gtc atc aag ctg gac cat aat acg cca 2933
 Glu Asp Asp Met Thr Val Ile Val Ile Lys Leu Asp His Asn Thr Pro
 800 805 810

aag tgg gcc tcc att ccg gcg ccg gct ttt ttc caa aag aat caa gag 2981
 Lys Trp Ala Ser Ile Pro Ala Pro Ala Phe Phe Gln Lys Asn Gln Glu
 815 820 825

att tct tagcattcgt ataaatcaaa tttcttctgg cgatgatgga actaaatcaa 3037
 Ile Ser

10295.204.ST25.txt

gatattctttg tccaggagga ataaaaacga tgaaaaaggg gcatttgaat caaatcctgc 3097
 ttttgacgga cggctgttca aaccgcggcg aagacccgca ggccatggct gcctttgcga 3157
 aagagcaggg aattaccgtg aatgtgattg ggattatgga cgagcatgaa atggatcagg 3217
 aggcgatgaa agaagtcgaa gggatcgctc tcgcaggcgg aggagttcac caggtgggtt 3277
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 ttcaaggcgt ggtcaacagt gagtcaaac aaattctcgg caagcatacc gaaatggatg 3397
 aactgcctcc tgataaacgc ggtgaagtca tggaagtcgt tgacgagctt ggtgagaccg 3457
 tgcattctca tgtactgggt cttgtcgata caa 3490

<210> 49
 <211> 829
 <212> PRT
 <213> Bacillus licheniformis

<400> 49

Met Glu Lys Ala Glu Arg Arg Val Asn Ser Pro Ile Ala Gly Pro Ala
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Val Gln Lys Leu Tyr Ser Trp Phe Gly Ser Met Thr Lys Leu Met Met
 20 25 30

Gln His Leu Tyr Ser Leu Phe Phe Tyr Lys Gly Leu Ile Tyr Met Val
 35 40 45

Ile Gly Phe Leu Leu Gly Arg Ala Phe Ile Leu Ser Glu Val Ile Pro
 50 55 60

Phe Ala Leu Pro Phe Phe Gly Ala Met Leu Leu Ile Lys Lys Asp Lys
 65 70 75 80

Ala Phe Leu Ala Cys Leu Ala Leu Leu Ala Gly Ala Leu Ser Ile Ser
 85 90 95

Pro Gln His Ser Leu Phe Val Leu Ala Ala Leu Phe Ala Phe Ala Ile
 100 105 110

Cys Ser Lys Met Thr Ser Leu Ile Ile Lys Asp Arg Val Arg Thr Leu
 115 120 125

Pro Val Val Val Phe Leu Ala Met Ala Val Thr Arg Cys Gly Phe Val
 130 135 140

Tyr Ala Glu Tyr Gly Thr Val Ser Gly Tyr His Tyr Ile Met Ala Phe
 145 150 155 160

Val Glu Ala Gly Leu Ser Phe Ile Leu Thr Leu Ile Phe Leu Gln Ser
 165 170 175

10295.204.ST25.txt

Leu Pro Ile Val Thr Ser Lys Arg Ala Lys Gln Ser Leu Lys Ile Glu
 180 185 190

Glu Ile Ile Cys Phe Met Ile Leu Ile Ala Ser Val Leu Thr Gly Leu
 195 200 205

Thr Gly Val Ser Phe Gln Gly Met Gln Ala Glu Leu Ile Leu Ala Arg
 210 215 220

Tyr Val Val Leu Ala Phe Ala Phe Ile Gly Gly Ala Ser Ile Gly Cys
 225 230 235 240

Thr Val Gly Val Val Thr Gly Leu Ile Leu Ser Leu Ser Asn Ile Gly
 245 250 255

Asn Leu Tyr Gln Met Ser Leu Leu Ala Phe Ser Gly Leu Leu Gly Gly
 260 265 270

Leu Leu Lys Glu Gly Lys Lys Phe Gly Ala Ala Val Gly Leu Leu Ile
 275 280 285

Gly Ser Leu Leu Ile Ser Leu Tyr Gly Glu Gly Ser Ala Glu Leu Val
 290 295 300

Pro Thr Leu Tyr Glu Ser Leu Ile Ala Ile Gly Leu Phe Leu Leu Thr
 305 310 315 320

Pro Gln Ser Ile Thr Lys Lys Val Ala Lys Tyr Ile Pro Gly Thr Thr
 325 330 335

Glu His Ala Gln Glu Gln Gln Gln Tyr Ala Arg Lys Ile Arg Asp Val
 340 345 350

Thr Ala Gln Lys Val Asp Gln Phe Ser Asn Val Phe His Ala Leu Ser
 355 360 365

Glu Ser Phe Ala Thr Phe Tyr His Ser Ala Pro Asp Asp Glu Gly Lys
 370 375 380

Glu Lys Glu Ile Asp Leu Phe Leu Ser Thr Val Thr Glu His Ser Cys
 385 390 395 400

Gln Ser Cys Tyr Lys Lys Asn Lys Cys Trp Val Gln Asn Phe Asp Lys
 405 410 415

Thr Tyr Asp Leu Met Lys Arg Val Met Gln Glu Thr Glu Glu Lys Gln
 420 425 430

Tyr Phe Lys Asn Arg Lys Leu Lys Lys Glu Phe His Gln His Cys Ser
 435 440 445

10295.204.ST25.txt

Lys Ser Lys Gln Val Glu Ala Leu Ile Glu Asp Glu Leu Thr His Phe
 450 455 460
 Arg Ala Asn Gln Thr Leu Lys Gln Lys Val His Asp Ser Arg Arg Leu
 465 470 475 480
 Val Ala Glu Gln Leu Leu Gly Val Ser Gln Val Met Ala Asp Phe Ser
 485 490 495
 Arg Glu Ile Lys Arg Glu Arg Glu Gln His Phe Ile Gln Glu Glu Gln
 500 505 510
 Ile Arg Asp Ala Leu Gln His Phe Gly Ile Glu Ile Gln Gln Val Glu
 515 520 525
 Ile Tyr Ser Leu Glu Gln Gly Asn Ile Asp Ile Glu Met Ser Ile Pro
 530 535 540
 Tyr Cys Asn Gly His Gly Glu Cys Glu Lys Ile Ile Ala Pro Met Leu
 545 550 555 560
 Ser Asp Ile Leu Glu Glu Gln Ile Ile Val Lys Ala Glu Gln Cys Ala
 565 570 575
 Gly His Pro Asn Gly Tyr Cys His Val Ala Phe Gly Ser Ala Lys Ser
 580 585 590
 Tyr Arg Val Val Thr Gly Ala Ala His Ala Ala Lys Gly Gly Gly Leu
 595 600 605
 Val Ser Gly Asp Ser Tyr Asn Met Met Glu Leu Gly Thr Gly Lys Tyr
 610 615 620
 Ala Ala Ala Ile Ser Asp Gly Met Gly Asn Gly Ala Arg Ala His Phe
 625 630 635 640
 Glu Ser Asn Glu Thr Ile Lys Leu Leu Glu Lys Ile Leu Gln Ser Gly
 645 650 655
 Ile Asp Glu Lys Val Ala Ile Lys Thr Ile Asn Ser Ile Leu Ser Leu
 660 665 670
 Arg Thr Thr Asp Glu Ile Tyr Ser Thr Leu Asp Leu Ser Val Ile Asp
 675 680 685
 Leu Gln Asp Ala Ser Cys Lys Phe Leu Lys Ile Gly Ser Thr Pro Ser
 690 695 700
 Phe Ile Lys Arg Gly Asp Gln Ile Ile Lys Val Gln Ala Ser Asn Leu
 705 710 715 720

10295.204.ST25.txt

Pro Ile Gly Ile Ile Thr Glu Phe Asp Val Asp Val Val Ser Glu Gln
725 730 735

Leu Lys Ala Gly Asp Leu Leu Ile Met Met Ser Asp Gly Ile Phe Glu
740 745 750

Gly Pro Arg His Val Glu Asn His Asp Leu Trp Met Lys Arg Lys Leu
755 760 765

Lys Ser Leu Lys Thr Glu Glu Pro Gln Glu Ile Ala Asp Leu Ile Met
770 775 780

Glu Glu Val Ile Arg Thr Arg Ser Gly Leu Ile Glu Asp Asp Met Thr
785 790 795 800

Val Ile Val Ile Lys Leu Asp His Asn Thr Pro Lys Trp Ala Ser Ile
805 810 815

Pro Ala Pro Ala Phe Phe Gln Lys Asn Gln Glu Ile Ser
820 825

<210> 50
<211> 1928
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1427)

<400> 50
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ttcaaaaccg ctgcccacaaa cgtaacggag ctgccgatca gagaagtctc aaaaggaaaa 180
tatgaaggat attggaccgc tacttcaact gcaaaagcaa aaggagcgga aatcgaggtc 240
atcgtcagag atgattacgg caatgaaacg agacaaacgg caaaaggcaa gctgtatatc 300
aatgaaaagc tgaaataaag gtgaaaagac gctgtcttta atggcagcgt ttttttcggt 360
ttacgatcga caaattcagt acgaaaactt caaaaaatgt acgatttacg caacattaat 420
tgacagactt tacctttggg cttgatttat acttaggaaa acaaacacta aggtcaccga 480
gccgcagaaa ggggaaggat gtg gaa atc tat tta gat gcg ata tgg ctg tta 533
Val Glu Ile Tyr Leu Asp Ala Ile Trp Leu Leu 10
aac ttt tgt ttt gac ttg ctg ctt tta atg atg acc gca ttt att tta 581
Asn Phe Cys Phe Asp Leu Leu Leu Leu Met Met Thr Ala Phe Ile Leu 25
aag cga agg gtt aaa aag cgg agg ctg atc cta ggg gca ttt gtc gcg 629
Lys Arg Arg Val Lys Lys Arg Arg Leu Ile Leu Gly Ala Phe Val Ala 40
30 35 40

10295.204.ST25.txt

tca agc atc gtt ctg ttt atg ttt aca cct ttt tca ccg tac gtc ctt Ser Ser Ile Val Leu Phe Met Phe Thr Pro Phe Ser Pro Tyr Val Leu 45 50 55	677
cat cct gcc ggc aaa ctg tcg ttt tcg gtt gtg atc gtt ctt gtg gca His Pro Ala Gly Lys Leu Ser Phe Ser Val Val Ile Val Leu Val Ala 60 65 70 75	725
ttt ggt ttt aag cgg ttc cgg ttt ttt ttg cag aat ttg ttt tct ttt Phe Gly Phe Lys Arg Phe Arg Phe Phe Leu Gln Asn Leu Phe Ser Phe 80 85 90	773
tat ttt gcc act ttt tta atg gga gga ggg att atc gga gcg cat tct Tyr Phe Ala Thr Phe Leu Met Gly Gly Gly Ile Ile Gly Ala His Ser 95 100 105	821
ttg ctt gaa acg gat tcg atc atg gaa aac ggc gtc ttt atg acg aat Leu Leu Glu Thr Asp Ser Ile Met Glu Asn Gly Val Phe Met Thr Asn 110 115 120	869
tgg tcc ggt ttt gga gac ccc gtc agc tgg ctg ttt gtc tgt gtg ggt Trp Ser Gly Phe Gly Asp Pro Val Ser Trp Leu Phe Val Cys Val Gly 125 130 135	917
ttt gcg gct gta tgg ctg ttt tca aaa aag cgt ttt gaa gat gct gaa Phe Ala Ala Val Trp Leu Phe Ser Lys Lys Arg Phe Glu Asp Ala Glu 140 145 150 155	965
gcg aag aaa att caa tac gaa gaa cgc gtc cgc cta gag gcc tgc att Ala Lys Lys Ile Gln Tyr Glu Glu Arg Val Arg Leu Glu Ala Cys Ile 160 165 170	1013
ggt gaa cat acg ctt cat ttc acc gga ttg att gac tcc gga aac cag Gly Glu His Thr Leu His Phe Thr Gly Leu Ile Asp Ser Gly Asn Gln 175 180 185	1061
ctc tac gat cca atc aca aaa acg ccc gtc atg atc gtc aat att gaa Leu Tyr Asp Pro Ile Thr Lys Thr Pro Val Met Ile Val Asn Ile Glu 190 195 200	1109
aaa ttg aaa gtt gta ttg gga gaa gag gca agt gtg acc atc aag gaa Lys Leu Lys Val Val Leu Gly Glu Glu Ala Ser Val Thr Ile Lys Glu 205 210 215	1157
atg agc ccg ctt gat gcc gtc ggg aaa ctg gat gaa gca ctg ccg tat Met Ser Pro Leu Asp Ala Val Gly Lys Leu Asp Glu Ala Leu Pro Tyr 220 225 230 235	1205
atc ggg cgg atc cgc ctg att ccg tac cgc ggg gtc ggc cat cag cat Ile Gly Arg Ile Arg Leu Ile Pro Tyr Arg Gly Val Gly His Gln His 240 245 250	1253
cag ttt ctg ctc tgc tta aag ccg gat cat gtg ctc gtt tgt acg gaa Gln Phe Leu Leu Cys Leu Lys Pro Asp His Val Leu Val Cys Thr Glu 255 260 265	1301
aga gaa gtg att gaa gcg ccg aaa tgc ctg att ggc atc agc aca tca Arg Glu Val Ile Glu Ala Pro Lys Cys Leu Ile Gly Ile Ser Thr Ser 270 275 280	1349
ccg ctt tcc gct gac ggc gaa ttt gac gcc atc gtc cat ccg aaa atg Pro Leu Ser Ala Asp Gly Glu Phe Asp Ala Ile Val His Pro Lys Met 285 290 295	1397
ctg gcc gga aac ccg gtc aaa cac gtt tct taaacttgaa gtctgttaca Leu Ala Gly Asn Pro Val Lys His Val Ser 300 305	1447

10295.204.ST25.txt

ttatcatact cctgaagacg tttattttaga aggggggagga agatgaaaaa actaaaatta 1507
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 tattatatcg gcggaagcga ggcgcttccc ccgccattgt caaaagatga agagcagggtg 1627
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 aaaatcaaac tggctacata tgcttcaga tgcattgaaa atgaaatttt gatgtattta 1867
 agaagaaaca ataaaatccg ttcagaggta tcattcgacg aaccgctgaa catcgattgg 1927
 1928

g

<210> 51
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 <213> Bacillus licheniformis

<400> 51

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Lys Arg Arg Leu Ile Leu Gly Ala Phe Val Ala Ser Ser Ile Val Leu
 35 40 45

Phe Met Phe Thr Pro Phe Ser Pro Tyr Val Leu His Pro Ala Gly Lys
 50 55 60

Leu Ser Phe Ser Val Val Ile Val Leu Val Ala Phe Gly Phe Lys Arg
 65 70 75 80

Phe Arg Phe Phe Leu Gln Asn Leu Phe Ser Phe Tyr Phe Ala Thr Phe
 85 90 95

Leu Met Gly Gly Gly Ile Ile Gly Ala His Ser Leu Leu Glu Thr Asp
 100 105 110

Ser Ile Met Glu Asn Gly Val Phe Met Thr Asn Trp Ser Gly Phe Gly
 115 120 125

Asp Pro Val Ser Trp Leu Phe Val Cys Val Gly Phe Ala Ala Val Trp
 130 135 140

Leu Phe Ser Lys Lys Arg Phe Glu Asp Ala Glu Ala Lys Lys Ile Gln
 145 150 155 160

Tyr Glu Glu Arg Val Arg Leu Glu Ala Cys Ile Gly Glu His Thr Leu
 165 170 175

10295.204.ST25.txt

His Phe Thr Gly Leu Ile Asp Ser Gly Asn Gln Leu Tyr Asp Pro Ile
 180 185 190

Thr Lys Thr Pro Val Met Ile Val Asn Ile Glu Lys Leu Lys Val Val
 195 200 205

Leu Gly Glu Glu Ala Ser Val Thr Ile Lys Glu Met Ser Pro Leu Asp
 210 215 220

Ala Val Gly Lys Leu Asp Glu Ala Leu Pro Tyr Ile Gly Arg Ile Arg
 225 230 235 240

Leu Ile Pro Tyr Arg Gly Val Gly His Gln His Gln Phe Leu Leu Cys
 245 250 255

Leu Lys Pro Asp His Val Leu Val Cys Thr Glu Arg Glu Val Ile Glu
 260 265 270

Ala Pro Lys Cys Leu Ile Gly Ile Ser Thr Ser Pro Leu Ser Ala Asp
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Gly Glu Phe Asp Ala Ile Val His Pro Lys Met Leu Ala Gly Asn Pro
 290 295 300

Val Lys His Val Ser
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 taagatcatg aagcttttct ttggacaagt caatccgacg gttttgacaa tggcggcggt 180
 aagggtggta tcatctttga tcgaactgac ggcggctgtt gtgatgcttt tgacaaacga 240
 cgtcagaaaa gctgtggcgg tcaacagcgt actggccatg gtcgggcccgc tcatctttat 300
 tattacaatg acaatcggca tctatcagat tgcagggcag ctttcttacg caaagctgat 360
 tttgatcttt atgggagtgg tttgatcat cgcggggatc tataaatagc gacacatgat 420
 aagagaggcc gactgtgcat aatgtcttcc tttgatcata catttttata gaagacaagc 480
 aaaaagagga gggagtgttt ttg cac cac atc aca gag att ctc ccc gat acg 533
 Leu His His Ile Thr Glu Ile Leu Pro Asp Thr
 1 5 10

10295.204.ST25.txt

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gaa gaa att cgg gtt cgg aca agt cgt ccg ctg gaa ctg gtg aac aaa Glu Glu Ile Arg Val Arg Thr Ser Arg Pro Leu Glu Leu Val Asn Lys 30 35 40	629
gga aag ccg cgc ttt ctc cct tat gtg gcg acg cct gaa gac tcg gcg Gly Lys Pro Arg Phe Leu Pro Tyr Val Ala Thr Pro Glu Asp Ser Ala 45 50 55	677
ctt ctt tta aac aga ttg gga aat tac agc atg tat aca ctg gaa gag Leu Leu Leu Asn Arg Leu Gly Asn Tyr Ser Met Tyr Thr Leu Glu Glu 60 65 70 75	725
gaa ttg aaa aaa gga tat gtc acg atc aga ggc gga cac cgc gtg ggg Glu Leu Lys Lys Gly Tyr Val Thr Ile Arg Gly Gly His Arg Val Gly 80 85 90	773
ctt gcc ggc cgg gtt gtc gtc gaa aac ggg gcc gtc aaa gga atc aga Leu Ala Gly Arg Val Val Val Glu Asn Gly Ala Val Lys Gly Ile Arg 95 100 105	821
gaa ata tca tca ttt aat att cgc att gcc aaa gaa aaa atc ggc att Glu Ile Ser Ser Phe Asn Ile Arg Ile Ala Lys Glu Lys Ile Gly Ile 110 115 120	869
tcc aaa ccg tat gtc ccc cat tta ttt caa aac tcg tgg ctg aac acg Ser Lys Pro Tyr Val Pro His Leu Phe Gln Asn Ser Trp Leu Asn Thr 125 130 135	917
ctg att atc ggt ccg ccg caa acc gga aaa aca aca ctg ctc aga gac Leu Ile Ile Gly Pro Pro Gln Thr Gly Lys Thr Thr Leu Leu Arg Asp 140 145 150 155	965
ctc gcc agg ctg atc agt tcg gga agc ggc aac gcc cct gcc aaa aaa Leu Ala Arg Leu Ile Ser Ser Gly Ser Gly Asn Ala Pro Ala Lys Lys 160 165 170	1013
gtg ggg att gtt gac gaa agg tct gaa atc gca ggc tgt gta aac ggc Val Gly Ile Val Asp Glu Arg Ser Glu Ile Ala Gly Cys Val Asn Gly 175 180 185	1061
ata ccg caa tat cgg ctc ggc gac cgg gca gac atc ctt gac gcc tgt Ile Pro Gln Tyr Arg Leu Gly Asp Arg Ala Asp Ile Leu Asp Ala Cys 190 195 200	1109
cca aaa gcg gaa ggg ctg atg atg atg atc aga tcg atg agt ccg gag Pro Lys Ala Glu Gly Leu Met Met Met Ile Arg Ser Met Ser Pro Glu 205 210 215	1157
gta atg atc gcc gat gag atc ggg aga atg gaa gac gca gaa gcg ctc Val Met Ile Ala Asp Glu Ile Gly Arg Met Glu Asp Ala Glu Ala Leu 220 225 230 235	1205
ttg gaa gcg gtc cac gcg ggg gtg act gtc atc gtt tcg gct cac ggc Leu Glu Ala Val His Ala Gly Val Thr Val Ile Val Ser Ala His Gly 240 245 250	1253
tac aca tat gca gat ctc gcc agg cgt cca tca ttg aaa atg ctt caa Tyr Thr Tyr Ala Asp Leu Ala Arg Arg Pro Ser Leu Lys Met Leu Gln 255 260 265	1301
gag cac cgg gtt ttt gag cga atc gtg gaa ctt tcc aga aag aac ggt Glu His Arg Val Phe Glu Arg Ile Val Glu Leu Ser Arg Lys Asn Gly 270 275 280	1349

10295.204.ST25.txt

ccc ggc agc ctg agc cgc atc cta aat ggg aac gga gag ccg ctc ggg 1397
 Pro Gly Ser Leu Ser Arg Ile Leu Asn Gly Asn Gly Glu Pro Leu Gly
 285 290 295
 gca gca aag agg atg tta tca tgc tgaagctttt aggtgccgtg cttattttgg 1451
 Ala Ala Lys Arg Met Leu Ser Cys
 300 305
 cagcagccac atggacagga ttgaaatgg cgaagccttt cagggaaagg ccgaagcaaa 1511
 tccgccagct gttggccgct ttgcagtctt tggaggctga aatcatgtac gggcatacac 1571
 cgctccgtca ggcatacaaaa cagatcgcac accagcttac cgagccggta gcctctttgt 1631
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 tggcgttaac ccatttagag acagaggaag ctgaagcaaa tctcgcccag gcgaaaaaatg 1871
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<210> 53
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 <212> PRT
 <213> Bacillus licheniformis

<400> 53

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 20 25 30

Arg Thr Ser Arg Pro Leu Glu Leu Val Asn Lys Gly Lys Pro Arg Phe
 35 40 45

Leu Pro Tyr Val Ala Thr Pro Glu Asp Ser Ala Leu Leu Leu Asn Arg
 50 55 60

Leu Gly Asn Tyr Ser Met Tyr Thr Leu Glu Glu Glu Leu Lys Lys Gly
 65 70 75 80

Tyr Val Thr Ile Arg Gly Gly His Arg Val Gly Leu Ala Gly Arg Val
 85 90 95

Val Val Glu Asn Gly Ala Val Lys Gly Ile Arg Glu Ile Ser Ser Phe
 100 105 110

Asn Ile Arg Ile Ala Lys Glu Lys Ile Gly Ile Ser Lys Pro Tyr Val
 115 120 125

Pro His Leu Phe Gln Asn Ser Trp Leu Asn Thr Leu Ile Ile Gly Pro
 130 135 140

10295.204.ST25.txt

Pro Gln Thr Gly Lys Thr Thr Leu Leu Arg Asp Leu Ala Arg Leu Ile
 145 150 155 160
 Ser Ser Gly Ser Gly Asn Ala Pro Ala Lys Lys Val Gly Ile Val Asp
 165 170 175
 Glu Arg Ser Glu Ile Ala Gly Cys Val Asn Gly Ile Pro Gln Tyr Arg
 180 185 190
 Leu Gly Asp Arg Ala Asp Ile Leu Asp Ala Cys Pro Lys Ala Glu Gly
 195 200 205
 Leu Met Met Met Ile Arg Ser Met Ser Pro Glu Val Met Ile Ala Asp
 210 215 220
 Glu Ile Gly Arg Met Glu Asp Ala Glu Ala Leu Leu Glu Ala Val His
 225 230 235 240
 Ala Gly Val Thr Val Ile Val Ser Ala His Gly Tyr Thr Tyr Ala Asp
 245 250 255
 Leu Ala Arg Arg Pro Ser Leu Lys Met Leu Gln Glu His Arg Val Phe
 260 265 270
 Glu Arg Ile Val Glu Leu Ser Arg Lys Asn Gly Pro Gly Ser Leu Ser
 275 280 285
 Arg Ile Leu Asn Gly Asn Gly Glu Pro Leu Gly Ala Ala Lys Arg Met
 290 295 300
 Leu Ser Cys
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<220>
 <221> CDS
 <222> (1036)..(1239)

<220>
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 <222> (1255)..(1509)

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 agttcgggaa gcggcaacgc ccctgcaaaa aaagtgggga ttgttgacga aaggctctgaa 120

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10295.204.ST25.txt

ttc att tat ata ttg ttc atg gtg gca act gtt gtc gat gat cta ttc 1206
 Phe Ile Tyr Ile Leu Phe Met Val Ala Thr Val Val Asp Asp Leu Phe
 215 220 225
 caa aag ata aaa gct gtc ttt cta ttt caa gga taggggggct cactc att 1257
 Gln Lys Ile Lys Ala Val Phe Leu Phe Gln Gly Ile
 230 235 240
 gaa atc gtt caa atc gta gga ctg gga atg atc gcc acc ttc ctc agc 1305
 Glu Ile Val Gln Ile Val Gly Leu Gly Met Ile Ala Thr Phe Leu Ser
 245 250 255
 ttg att gtg aaa gag caa aaa ccg acg ttt gct ttt ttg att gtc gtt 1353
 Leu Ile Val Lys Glu Gln Lys Pro Thr Phe Ala Phe Leu Ile Val Val
 260 265 270
 ttt gcc ggc tgc acg att ttt tta ttc tta gta gat cag gtc tac gaa 1401
 Phe Ala Gly Cys Thr Ile Phe Leu Phe Leu Val Asp Gln Val Tyr Glu
 275 280 285
 atc att cgg atg att gaa aaa ata gct gcc aat gcc aac atc aac atg 1449
 Ile Ile Arg Met Ile Glu Lys Ile Ala Ala Asn Ala Asn Ile Asn Met
 290 295 300
 atg tat gtc gaa acg att ttg aag att atc ggg att gct tat att gcg 1497
 Met Tyr Val Glu Thr Ile Leu Lys Ile Ile Gly Ile Ala Tyr Ile Ala
 305 310 315 320
 gag ttt ggc gcc ca 1511
 Glu Phe Gly Ala

<210> 55
 <211> 171
 <212> PRT
 <213> Bacillus licheniformis

<400> 55

Met Leu Lys Leu Leu Gly Ala Val Leu Ile Leu Ala Ala Ala Thr Trp
 1 5 10 15

Thr Gly Phe Glu Met Ala Lys Pro Phe Arg Glu Arg Pro Lys Gln Ile
 20 25 30

Arg Gln Leu Leu Ala Ala Leu Gln Ser Leu Glu Ala Glu Ile Met Tyr
 35 40 45

Gly His Thr Pro Leu Arg Gln Ala Ser Lys Gln Ile Ala His Gln Leu
 50 55 60

Thr Glu Pro Val Ala Ser Leu Phe Gln Thr Phe Ala Glu Gln Leu Glu
 65 70 75 80

Lys Gly Ser Ala Ser Ala Gly Thr Ala Trp Glu Asp Ser Leu Glu Lys
 85 90 95

Val Trp Pro Glu Thr Ala Leu Lys Lys Lys Glu Tyr Glu Ile Leu Arg
 100 105 110

10295.204.ST25.txt

Gln Phe Gly Glu Thr Leu Gly Arg His Asp Leu Ile Ser Gln Gln Lys
 115 120 125

His Ile Lys Leu Ala Leu Thr His Leu Glu Thr Glu Glu Ala Glu Ala
 130 135 140

Asn Leu Ala Gln Ala Lys Asn Glu Lys Met Val Lys Ser Leu Gly Phe
 145 150 155 160

Leu Thr Gly Leu Leu Ile Leu Leu Leu Met
 165 170

<210> 56
 <211> 68
 <212> PRT
 <213> Bacillus licheniformis

<400> 56

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Val Val Ala Phe Leu His Thr Ile Leu Asp Gln Met Gly Lys Lys Glu
 20 25 30

Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile Tyr Ile Leu Phe Met
 35 40 45

Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys Ile Lys Ala Val Phe
 50 55 60

Leu Phe Gln Gly
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<210> 57
 <211> 85
 <212> PRT
 <213> Bacillus licheniformis

<400> 57

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Ser Leu Ile Val Lys Glu Gln Lys Pro Thr Phe Ala Phe Leu Ile Val
 20 25 30

Val Phe Ala Gly Cys Thr Ile Phe Leu Phe Leu Val Asp Gln Val Tyr
 35 40 45

Glu Ile Ile Arg Met Ile Glu Lys Ile Ala Ala Asn Ala Asn Ile Asn
 50 55 60

Met Met Tyr Val Glu Thr Ile Leu Lys Ile Ile Gly Ile Ala Tyr Ile
 65 70 75 80

Ala Glu Phe Gly Ala
85

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<210> 58
<211> 1207
<212> DNA
<213> Bacillus licheniformis
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<221> CDS
<222> (501) .. (704)
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15 20 25

atg ggg aag aag gaa tat gcc caa tgg gtc acg ctt tta gga ttc att 629
Met Gly Lys Lys Glu Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile
30 35 40

tat ata ttg ttc atg gtg gca act gtt gtc gat gat cta ttc caa aag 677
Tyr Ile Leu Phe Met Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys
45 50 55

ata aaa gct gtc ttt cta ttt caa gga taggggggct cactcattga 724
ile Lys Ala Val Phe Leu Phe Gln Gly
60 65

aatcgttcaa atcgtaggac tgggaatgat cgccaccttc ctcagcttga ttgtgaaaga 784

gcaaaaaccg. acgtttgctt ttttgattgt cgtttttgcc. ggctgcacga tttttttatt 844

cttagtagat caggtctacg aaatcattcg gatgattgaa aaaatagctg ccaatgccaa -- 904

catcaacatg atgtatgtcg aaacgatttt gaagattatc gggattgctt atattgcgga 964

gtttggcgcc cagctgacaa aggatgccgg acagggtgcg attgcttcga agatcgaatt 1024

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gatcatcgga ctcatccctt ccatgtctta gtcagaaagg aggatttcct gagtgaagcg 1144

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10295.204.ST25.txt

1207

ttc

<210> 59
 <211> 68
 <212> PRT
 <213> Bacillus licheniformis

<400> 59

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 20 25 30

Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile Tyr Ile Leu Phe Met
 35 40 45

Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys Ile Lys Ala Val Phe
 50 55 60

Leu Phe Gln Gly
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 tgcctatttt aaccgtgatt atcgaaacga tcatcggact catcccttcc atgtcttagt 480
 cagaaaggag gatttcctga gtg aag cgt ttt ctg ttc tgg ctc ttg gtc atc 533
 Val Lys Arg Phe Leu Phe Trp Leu Leu Val Ile 10
 gga atc gta tgc ttt gga gcg cat aat gta caa gct tcg cca aaa gaa 581
 Gly Ile Val Cys Phe Gly Ala His Asn Val Gln Ala Ser Pro Lys Glu 25
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 Ala Glu Pro Ala Gly Glu Thr Ala Ala Glu Glu Ser Ala Glu Ala Ile

10295.204.ST25.txt

30	35	40	
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tgg aac aac att ttg aca gag tat ggg gga cac ctt ccc gaa agt caa Trp Asn Asn Ile Leu Thr Glu Tyr Gly Gly His Leu Pro Glu Ser Gln 60 65 70 75			725
aaa gga agc ctg ctt gaa ttt gtc aaa gga gaa aag cac ttt tcg cct Lys Gly Ser Leu Leu Glu Phe Val Lys Gly Glu Lys His Phe Ser Pro 80 85 90			773
gag gaa tgg ggc aaa gcg ctg ttt tcc tac ttg ttc cat gaa gtg ctg Glu Glu Trp Gly Lys Ala Leu Phe Ser Tyr Leu Phe His Glu Val Leu 95 100 105			821
gct aac ggg aaa ctg ctg ggg acg ctg atc ctg ttg acc atc ttc tgc Ala Asn Gly Lys Leu Leu Gly Thr Leu Ile Leu Leu Thr Ile Phe Cys 110 115 120			869
gtc ctg ctt cag ctt ttg caa aac gcg ttt caa caa agc acc gtc agc Val Leu Leu Gln Leu Leu Gln Asn Ala Phe Gln Gln Ser Thr Val Ser 125 130 135			917
aaa gtg gcg tat gca att gtc tac atg gtg ctg att att ctt gcg ctc Lys Val Ala Tyr Ala Ile Val Tyr Met Val Leu Ile Ile Leu Ala Leu 140 145 150 155			965
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atg aca agc ttt atc ctg tcg ctc gta cct ctg ctt ctg gcg ctg atg Met Thr Ser Phe Ile Leu Ser Leu Val Pro Leu Leu Leu Ala Leu Met 175 180 185			1061
gcg act tcg ggg gga gcc gcc tca gcc gca ttc ttt cat ccg gtc att Ala Thr Ser Gly Gly Ala Ala Ser Ala Ala Phe Phe His Pro Val Ile 190 195 200			1109
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ccg ctt tta ttt tta tca gcg att tta agc att gtc agc acg atg acg Pro Leu Leu Phe Leu Ser Ala Ile Leu Ser Ile Val Ser Thr Met Thr 220 225 230 235			1205
gac caa tat aaa gtc aca cag ctg gcc cag ctc ctc aga aat gcg gcg Asp Gln Tyr Lys Val Thr Gln Leu Ala Gln Leu Leu Arg Asn Ala Ala 240 245 250			1253
atc ggc acg ctg gct gca ttt ttg acc gta ttc ctc ggt gtc atc tcg Ile Gly Thr Leu Ala Ala Phe Leu Thr Val Phe Leu Gly Val Ile Ser 255 260 265			1301
gtt cag ggc gcc tca gcc gca gtg acg gac ggc att act ttg cgg acg Val Gln Gly Ala Ser Ala Ala Val Thr Asp Gly Ile Thr Leu Arg Thr 270 275 280			1349
gca aaa ttc att acc gga aac ttc atc ccc gta ttg ggc cgc atg ttt Ala Lys Phe Ile Thr Gly Asn Phe Ile Pro Val Leu Gly Arg Met Phe 285 290 295			1397
acc gaa gcg aca gac acg gtg atc agc gcg tct ctc ctg ctg aaa aac Thr Glu Ala Thr Asp Thr Val Ile Ser Ala Ser Leu Leu Leu Lys Asn 300 305 310 315 320 325 330 335 340 345 350			1445

10295.204.ST25.txt
310

300 305 315
 acc gtc ggg ata ctc ggt gtg gca atc tta att tgc atc gca gcc ttt 1493
 Thr Val Gly Ile Leu Gly Val Ala Ile Leu Ile Cys Ile Ala Ala Phe
 320 325 330
 ccc gcg atc aaa atc ctt tcc ctc gcg ctc ata tac aaa att gcc gcg 1541
 Pro Ala Ile Lys Ile Leu Ser Leu Ala Leu Ile Tyr Lys Ile Ala Ala
 335 340 345
 gcg gtt ctc cag cct ctc gga ggc ggc ccg gtt atc agc tgc ctg gat 1589
 Ala Val Leu Gln Pro Leu Gly Gly Gly Pro Val Ile Ser Cys Leu Asp
 350 355 360
 gtc atc agc aaa agc gtc atc tac att ttc gcg gcc atg gcc atc gtt 1637
 Val Ile Ser Lys Ser Val Ile Tyr Ile Phe Ala Ala Met Ala Ile Val
 365 370 375
 tcg ctg atg ttt ttc tta agc tta acc gtg atc att aca gcg ggg aat 1685
 Ser Leu Met Phe Phe Leu Ser Leu Thr Val Ile Ile Thr Ala Gly Asn
 380 385 390 395
 ctg acg atg atg atg aag tagggagggg tgagatggaa tttctgacag 1733
 Leu Thr Met Met Met Lys 400
 agtggctcac gaatattatt ctatttattc tgatggcgat cgtcatcgat atgcttctgc 1793
 cgaattcgag catgcaaaaa tacgcgaaaa tgggtgatcag cctgctcttg atcgttgtaa 1853
 tactgaaccc gatcttctct ttattcagga cagatccgga tgtgattttt gagaagctta 1913
 caaaaaacgg acaagttcag tcaaacgaaa taaaaaatca gctgaattca gaaaaaaaag 1973
 aaatacaagc ctcacaacaa gcatatatct tagaacagat ggctgttcaa ttggaaaaga 2033
 acgcagaggg caggttttaca agcgacaaat acaagataga ccgagtcgag gtctcttctg 2093
 acagccagct gaaaacagag aaagacctca gtaagcatgc ggaagtctcg gtattcttga 2153
 <210> 61
 <211> 401
 <212> PRT
 <213> Bacillus licheniformis
 <400> 61
 Val Lys Arg Phe Leu Phe Trp Leu Leu Val Ile Gly Ile Val Cys Phe
 1 5 10 15
 Gly Ala His Asn Val Gln Ala Ser Pro Lys Glu Ala Glu Pro Ala Gly
 20 25 30
 Glu Thr Ala Ala Glu Glu Ser Ala Glu Ala Ile Ala Arg Glu Gln Ala
 35 40 45
 Glu Gly Leu Glu Leu Asp Arg Val Gly Glu Phe Trp Asn Asn Ile Leu
 50 55 60
 Thr Glu Tyr Gly Gly His Leu Pro Glu Ser Gln Lys Gly Ser Leu Leu
 65 70 75 80

10295.204.ST25.txt

Glu Phe Val Lys Gly Glu Lys His Phe Ser Pro Glu Glu Trp Gly Lys
 85 90 95
 Ala Leu Phe Ser Tyr Leu Phe His Glu Val Leu Ala Asn Gly Lys Leu
 100 105 110
 Leu Gly Thr Leu Ile Leu Leu Thr Ile Phe Cys Val Leu Leu Gln Leu
 115 120 125
 Leu Gln Asn Ala Phe Gln Gln Ser Thr Val Ser Lys Val Ala Tyr Ala
 130 135 140
 Ile Val Tyr Met Val Leu Ile Ile Leu Ala Leu Asn Ser Phe Arg Val
 145 150 155 160
 Ala Val Thr Tyr Ala Asn Glu Ala Ile Gln Thr Met Thr Ser Phe Ile
 165 170 175
 Leu Ser Leu Val Pro Leu Leu Leu Ala Leu Met Ala Thr Ser Gly Gly
 180 185 190
 Ala Ala Ser Ala Ala Phe Phe His Pro Val Ile Leu Phe Leu Met Asn
 195 200 205
 Thr Ser Gly Leu Phe Ile Gln Tyr Ile Val Leu Pro Leu Leu Phe Leu
 210 215 220
 Ser Ala Ile Leu Ser Ile Val Ser Thr Met Thr Asp Gln Tyr Lys Val
 225 230 235 240
 Thr Gln Leu Ala Gln Leu Leu Arg Asn Ala Ala Ile Gly Thr Leu Ala
 245 250 255
 Ala Phe Leu Thr Val Phe Leu Gly Val Ile Ser Val Gln Gly Ala Ser
 260 265 270
 Ala Ala Val Thr Asp Gly Ile Thr Leu Arg Thr Ala Lys Phe Ile Thr
 275 280 285
 Gly Asn Phe Ile Pro Val Leu Gly Arg Met Phe Thr Glu Ala Thr Asp
 290 295 300
 Thr Val Ile Ser Ala Ser Leu Leu Leu Lys Asn Thr Val Gly Ile Leu
 305 310 315 320
 Gly Val Ala Ile Leu Ile Cys Ile Ala Ala Phe Pro Ala Ile Lys Ile
 325 330 335
 Leu Ser Leu Ala Leu Ile Tyr Lys Ile Ala Ala Ala Val Leu Gln Pro
 340 345 350

10295.204.ST25.txt

Leu Gly Gly Gly Pro Val Ile Ser Cys Leu Asp Val Ile Ser Lys Ser
 355 360 365

Val Ile Tyr Ile Phe Ala Ala Met Ala Ile Val Ser Leu Met Phe Phe
 370 375 380

Leu Ser Leu Thr Val Ile Ile Thr Ala Gly Asn Leu Thr Met Met Met
 385 390 395 400

Lys

<210> 62
 <211> 1696
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1193)

<400> 62
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 ttttgagaag cttacaaaaa acggacaagt tcagtcaaac gaaataaaaa atcagctgaa 120
 ttcagaaaaa aaagaaatac aagcctcaca acaagcatat atcttagaac agatggctgt 180
 tcaattggaa aagaacgcag agggcagggt tacaagcgac aaatacaaga tagaccgagt 240
 cgaggctctt tctgacagcc agctgaaaac agagaaagac ctcagtaagc atgcggaagt 300
 ctcggtattc ttgaaaccag catcggaaaa aacggtccaa gccgtcgctc ctgtcgagat 360
 caatacggac cggagctacc agtccatgca ggaaagagaa aagaaagaga cggggggaagt 420
 cagagaacag ctagcaggca tctgggaaat aagccccgac aagattacag ttcatatcga 480
 aggggggagaa cgaagcggca atg aat aaa aga acc tgg atc gaa aag ctg atc 533
 Met Asn Lys Arg Thr Trp Ile Glu Lys Leu Ile
 1 5 10
 ggc cac ctg ctc ccg aaa gac gag aaa gac gga aaa aag ctg acg aaa 581
 Gly His Leu Leu Pro Lys Asp Glu Lys Asp Gly Lys Lys Leu Thr Lys
 15 20 25
 tat cac tac ttt ctg ctg ctt ttt gtt ctc ggc gtt tcc ttc atg ctc 629
 Tyr His Tyr Phe Leu Leu Leu Phe Val Leu Gly Val Ser Phe Met Leu
 30 35 40
 gtc agc cag atc ttc tct tcc gaa cct tcc caa gag cca gcg gca gat 677
 Val Ser Gln Ile Phe Ser Ser Glu Pro Ser Gln Glu Pro Ala Ala Asp
 45 50 55
 cag ccg gcg gct tca caa aaa gct acg tct gaa agc acc gta cag agc 725
 Gln Pro Ala Ala Ser Gln Lys Ala Thr Ser Glu Ser Thr Val Gln Ser
 60 65 70 75
 ggt gaa gga gaa aaa gaa gtg ttc aag ccc gcc tca gat gac aaa ccg 773
 Gly Glu Gly Glu Lys Glu Val Phe Lys Pro Ala Ser Asp Asp Lys Pro
 80 85 90
 aag gaa tcg atc caa gat tac gaa cag gaa tat gaa aat cag ctc aaa 821

10295.204.ST25.txt

Lys Glu Ser Ile Gln Asp Tyr Glu Gln Glu Tyr Glu Asn Gln Leu Lys
 95 100 105
 gac ata ttg gaa acc atc atc ggc gtt gag gac gtg tca atc gtc gtc 869
 Asp Ile Leu Glu Thr Ile Ile Gly Val Glu Asp Val Ser Ile Val Val
 110 115 120
 aat gtt gat gca acc tca ttg aaa ata ttc gag aaa aac aga aaa acc 917
 Asn Val Asp Ala Thr Ser Leu Lys Ile Phe Glu Lys Asn Arg Lys Thr
 125 130 135
 cag gaa act tca acg aat gag aca gat aaa cag gga ggc aag cgg acg 965
 Gln Glu Thr Ser Thr Asn Glu Thr Asp Lys Gln Gly Gly Lys Arg Thr
 140 145 150 155
 gtg tct gaa atg tct tca gac gaa gaa atc gtc atc atc aaa aac gga 1013
 Val Ser Glu Met Ser Ser Asp Glu Glu Ile Val Ile Ile Lys Asn Gly
 160 165 170
 gat aaa gag acg cct gtc gtc gtt cag acg aaa aag ccc gat atc agg 1061
 Asp Lys Glu Thr Pro Val Val Val Gln Thr Lys Lys Pro Asp Ile Arg
 175 180 185
 ggt gtt ctc gtt gtc gct cag gga gtc gac aac gtt caa ata aaa aag 1109
 Gly Val Leu Val Val Ala Gln Gly Val Asp Asn Val Gln Ile Lys Lys
 190 195 200
 acc att att gaa gca gtg aca agg gtt ctt gat gtt ccg agc cac cgc 1157
 Thr Ile Ile Glu Ala Val Thr Arg Val Leu Asp Val Pro Ser His Arg
 205 210 215
 gtc gct gtt gcc cct aaa aaa atg aag gag gat tca taaatgatgc 1203
 Val Ala Val Ala Pro Lys Lys Met Lys Glu Asp Ser
 220 225 230
 tgaaaaaaca aacgggtttgg cttttaacca tgtaaagtct cgtcgttgta ctgagtgtct 1263
 actacattat gtcgcccgaa ggagaaaatg tcgtcacggt tgatgacaag gaacaagttg 1323
 ccgctgaaaa agaaaaaccg atgaaagaag agcctgccaa ggatggcaaa gatgataccg 1383
 cgcctgctaa agacaaaact aaagggaag atacaaaaga taaagaaacg tctgcgagtg 1443
 agcagaacgg agaggttgct acagaggaat catcgggtga tgaagattta ttcacaacat 1503
 accgcatgga aatggacgat cagcgcagca gggagagggg ggaattaacc gaaatcgtca 1563
 gaagcgataa agcgacggca aaagaaaaaa gcgaagctta cgacaagatg acagagctca 1623
 gcgaagctga aggaacggaa aagacccttg aaaccctcat caaaacaaaa ggctattaag 1683
 acgccttggt caa 1696

<210> 63
 <211> 231
 <212> PRT
 <213> Bacillus licheniformis

<400> 63

Met Asn Lys Arg Thr Trp Ile Glu Lys Leu Ile Gly His Leu Leu Pro
 1 5 10 15

Lys Asp Glu Lys Asp Gly Lys Lys Leu Thr Lys Tyr His Tyr Phe Leu
 20 25 30

10295.204.ST25.txt

Leu Leu Phe Val Leu Gly Val Ser Phe Met Leu Val Ser Gln Ile Phe
 35 40 45

Ser Ser Glu Pro Ser Gln Glu Pro Ala Ala Asp Gln Pro Ala Ala Ser
 50 55 60

Gln Lys Ala Thr Ser Glu Ser Thr Val Gln Ser Gly Glu Gly Glu Lys
 65 70 75 80

Glu Val Phe Lys Pro Ala Ser Asp Asp Lys Pro Lys Glu Ser Ile Gln
 85 90 95

Asp Tyr Glu Gln Glu Tyr Glu Asn Gln Leu Lys Asp Ile Leu Glu Thr
 100 105 110

Ile Ile Gly Val Glu Asp Val Ser Ile Val Val Asn Val Asp Ala Thr
 115 120 125

Ser Leu Lys Ile Phe Glu Lys Asn Arg Lys Thr Gln Glu Thr Ser Thr
 130 135 140

Asn Glu Thr Asp Lys Gln Gly Gly Lys Arg Thr Val Ser Glu Met Ser
 145 150 155 160

Ser Asp Glu Glu Ile Val Ile Ile Lys Asn Gly Asp Lys Glu Thr Pro
 165 170 175

Val Val Val Gln Thr Lys Lys Pro Asp Ile Arg Gly Val Leu Val Val
 180 185 190

Ala Gln Gly Val Asp Asn Val Gln Ile Lys Lys Thr Ile Ile Glu Ala
 195 200 205

Val Thr Arg Val Leu Asp Val Pro Ser His Arg Val Ala Val Ala Pro
 210 215 220

Lys Lys Met Lys Glu Asp Ser
 225 230

<210> 64
 <211> 1062
 <212> DNA
 <213> Bacillus-licheniformis

<220>
 <221> CDS
 <222> (498)..(980)

<400> 64
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 cagatgacaa accgaaggaa tcgatccaag attacgaaca ggaatatgaa aatcagctca 120

10295.204.ST25.txt

aagacatatt ggaaaccatc atcggcgttg aggacgtgtc aatcgtcgtc aatgttgatg 180
caacctcatt gaaaatattc gagaaaaaca gaaaaaccca ggaaacttca acgaatgaga 240
cagataaaca gggaggcaag cggacggtgt ctgaaatgtc ttcagacgaa gaaatcgtca 300
tcatcaaaaa cggagataaa gagacgcctg tcgtcgttca gacgaaaaag cccgatatca 360
ggggtgttct cgttgtcgct cagggagtcg acaacgttca aataaaaaag accattattg 420
aagcagtgc aagggttctt gatgttccga gccaccgcgt cgctgttgcc cctaaaaaaa 480
tgaaggagga ttcataa atg atg ctg aaa aaa caa acg gtt tgg ctt tta 530
Met Met Leu Lys Lys Gln Thr Val Trp Leu Leu
1 5 10
acc atg tta agt ctc gtc gtt gta ctg agt gtc tac tac att atg tcg 578
Thr Met Leu Ser Leu Val Val Val Leu Ser Val Tyr Tyr Ile Met Ser
15 20 25
ccc gaa gga gaa aat gtc gtc acg gtt gat gac aag gaa caa gtt gcc 626
Pro Glu Gly Glu Asn Val Val Thr Val Asp Asp Lys Glu Gln Val Ala
30 35 40
gct gaa aaa gaa aaa ccg atg aaa gaa gag cct gcc aag gat ggc aaa 674
Ala Glu Lys Glu Lys Pro Met Lys Glu Glu Pro Ala Lys Asp Gly Lys
45 50 55
gat gat acc gcg cct gct aaa gac aaa act aaa ggg aaa gat aca aaa 722
Asp Asp Thr Ala Pro Ala Lys Asp Lys Thr Lys Gly Lys Asp Thr Lys
60 65 70 75
gat aaa gaa acg tct gcg agt gag cag aac gga gag gtt gtc aca gag 770
Asp Lys Glu Thr Ser Ala Ser Glu Gln Asn Gly Glu Val Val Thr Glu
80 85 90
gaa tca tcg ggt gat gaa gat tta ttc aca aca tac cgc atg gaa atg 818
Glu Ser Ser Gly Asp Glu Asp Leu Phe Thr Thr Tyr Arg Met Glu Met
95 100 105
gac gat cag cgc agc agg gag agg gag gaa tta acc gaa atc gtc aga 866
Asp Asp Gln Arg Ser Arg Glu Arg Glu Glu Leu Thr Glu Ile Val Arg
110 115 120
agc gat aaa gcg acg gca aaa gaa aaa agc gaa gct tac gac aag atg 914
Ser Asp Lys Ala Thr Ala Lys Glu Lys Ser Glu Ala Tyr Asp Lys Met
125 130 135
aca gag ctc agc gaa gct gaa gga acg gaa aag acc ctt gaa acc ctc 962
Thr Glu Leu Ser Glu Ala Glu Gly Thr Glu Lys Thr Leu Glu Thr Leu
140 145 150 155
atc aaa aca aaa ggc tat taagacgcct tggtaacgc cgacggcgat 1010
Ile Lys Thr Lys Gly Tyr
160
aaagtcaata ttacggtgaa ggcgaaggag cactcgaaa cgcctgcac cg 1062

<210> 65
<211> 161
<212> PRT
<213> Bacillus licheniformis

<400> 65

Met Met Leu Lys Lys Gln Thr Val Trp Leu Leu Thr Met Leu Ser Leu
1 5 10 15

10295.204.ST25.txt

Val Val Val Leu Ser Val Tyr Tyr Ile Met Ser Pro Glu Gly Glu Asn
20 25 30

Val Val Thr Val Asp Asp Lys Glu Gln Val Ala Ala Glu Lys Glu Lys
35 40 45

Pro Met Lys Glu Glu Pro Ala Lys Asp Gly Lys Asp Asp Thr Ala Pro
50 55 60

Ala Lys Asp Lys Thr Lys Gly Lys Asp Thr Lys Asp Lys Glu Thr Ser
65 70 75 80

Ala Ser Glu Gln Asn Gly Glu Val Val Thr Glu Glu Ser Ser Gly Asp
85 90 95

Glu Asp Leu Phe Thr Thr Tyr Arg Met Glu Met Asp Asp Gln Arg Ser
100 105 110

Arg Glu Arg Glu Glu Leu Thr Glu Ile Val Arg Ser Asp Lys Ala Thr
115 120 125

Ala Lys Glu Lys Ser Glu Ala Tyr Asp Lys Met Thr Glu Leu Ser Glu
130 135 140

Ala Glu Gly Thr Glu Lys Thr Leu Glu Thr Leu Ile Lys Thr Lys Gly
145 150 155 160

Tyr

<210> 66
<211> 3346
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(2843)

<400> 66
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taaatacggg ttaatcgatg aaaaccggcg agagacagac aggcgattca aaagctgatg 120
aatataatcg aacaaaacaa ggacgcacag gaagagataa tccaatgatt ctgtataaaa 180
aaatgccgca ggaaatcgtg ttcgcagggc aggcggaaaa ctcgaactta aaacagatcg 240
atgtaaacag cgtaccactt ttagtcgaga tgaacggaga ggaagcaagg aacgttcaga 300
gttctcagca cgaacccgat ggatttttta aaacaagaaa cggcccctgg gcagacgctt 360
aaactgacat ttataaata gctggagtgt ctcaaggata aatatgctat aataggggaa 420
tccagaggaa aatcgacgcc gaaaaaggc tgctttctct ttgtttttac attttttaac 480

10295.204.ST25.txt

acgcagtaag gtgatggaac atg gca aaa aga aaa cga aaa tca aca aag aaa 533
Met Ala Lys Arg Lys Arg Lys Ser Thr Lys Lys
1 5 10

caa aaa caa gga aaa aaa cgg atc cat ctt aaa ttt gaa ttg tac gga 581
Gln Lys Gln Gly Lys Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly
15 20 25

tta atc tgt atc gcc atc tcg att att gcg gtt ttg cag ctt ggc gta 629
Leu Ile Cys Ile Ala Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val
30 35 40

gca ggg caa acg ttc att tac atg ttc cgc ttt ttc gcc ggt gaa tgg 677
Ala Gly Gln Thr Phe Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp
45 50 55

ttc atc ctt tgc ctt ctc ggc ctc ttt tta acg ggc ttg tct tta ttt 725
Phe Ile Leu Cys Leu Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe
60 65 70 75

tgg aaa aag aaa aca ccc agt ttt ttg acg agg aga aaa gcg ggc ctt 773
Trp Lys Lys Lys Thr Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu
80 85 90

tac tgc atc att gca agc atg ctg ctt ctt tca cat gtc cag ctg ttt 821
Tyr Cys Ile Ile Ala Ser Met Leu Leu Leu Ser His Val Gln Leu Phe
95 100 105

cag cat ttg acc gaa agg gga atg gtt cag tct ccg agc gtg atc caa 869
Gln His Leu Thr Glu Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln
110 115 120

aat acg tgg gag ctg ttt ctg atg gat gta aaa ggc gag aca gga tcg 917
Asn Thr Trp Glu Leu Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser
125 130 135

cct gat ctt gga ggc gga atg att gga gcc ctt tta ttc gcg gcg tca 965
Pro Asp Leu Gly Gly Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser
140 145 150 155

tat ttt ctg ttt gca tct gca gga tct aaa atc atc gcc gtc ttc ctg 1013
Tyr Phe Leu Phe Ala Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu
160 165 170

atc ttg atc ggc ctt ctt ttg att acg gat cgg tcg ctt cag gag acg 1061
Ile Leu Ile Gly Leu Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr
175 180 185

ctg atc aaa tgg atg acc ccg gtc gcc tcc ttc atg aaa aac cag tgg 1109
Leu Ile Lys Trp Met Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp
190 195 200

cag gcc ttt tta gca gat ctt aaa caa ttg aaa aac agc tcg ccg aaa 1157
Gln Ala Phe Leu Ala Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys
205 210 215

aag aaa tcc gga aaa aaa caa aag acg cag aga aaa ccg aaa gtg tct 1205
Lys Lys Ser Gly Lys Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser
220 225 230 235

gaa gag cct gta caa gaa gcg gac ctt gat cca gat ccg gtt att caa 1253
Glu Glu Pro Val Gln Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln
240 245 250

tca gaa ccg att att tca agc ttt tcc gac cgt gat gaa aag ccc gaa 1301
Ser Glu Pro Ile Ile Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu
255 260 265

10295.204.ST25.txt

gtt caa gct tac gaa gct ccg gcg gct cct gct gaa cct cct gct gag Val Gln Ala Tyr Glu Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu 270 275 280	1349
ccc gaa atc ggt gag gaa atg cag gcc tcc ggc gcg ccc gaa atc acg Pro Glu Ile Gly Glu Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr 285 290 295	1397
ttt aca gag cta gaa aac aag gat tac cag ctt ccg tcg att caa ttg Phe Thr Glu Leu Glu Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu 300 305 310 315	1445
ctg gat gat ccg aag cac aca ggg cag cag gcg gat aaa aag aat att Leu Asp Asp Pro Lys His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile 320 325 330	1493
tac gac aat gcc agg aag ctg gaa agg acg ttt caa agc ttc gga gtt Tyr Asp Asn Ala Arg Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val 335 340 345	1541
aag gcg aaa gtc acc cag gtt cat ctc ggc ccg gcc gtc acg aaa tat Lys Ala Lys Val Thr Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr 350 355 360	1589
gaa gtc tat cct gat gtg ggc gtc aaa gtc agc aaa att gtc aac tta Glu Val Tyr Pro Asp Val Gly Val Lys Val Ser Lys Ile Val Asn Leu 365 370 375	1637
agt gac gac ttg gct tta gcg ctc gcg gcc aag gat atc cgc atc gaa Ser Asp Asp Leu Ala Leu Ala Leu Ala Lys Asp Ile Arg Ile Glu 380 385 390 395	1685
gcc ccg atc ccc gga aaa tcg gcg att gga atc gaa gtg ccg aat gcg Ala Pro Ile Pro Gly Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala 400 405 410	1733
gaa gtg gcg atg gtt tcc ttg aaa gaa gtg ctt gaa tcg aaa ctg aat Glu Val Ala Met Val Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn 415 420 425	1781
gac cgg ccg gat gca aag ctg atg atc ggc ctc ggc cgg aac att tcc Asp Arg Pro Asp Ala Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser 430 435 440	1829
gga gaa gcg gta ttg gca gag ctg aac aaa atg ccc cac ctt ctt gtt Gly Glu Ala Val Leu Ala Glu Leu Asn Lys Met Pro His Leu Leu Val 445 450 455	1877
gca gga gcg acc gga agc ggg aaa agc gtc tgt gtc aac ggg atc att Ala Gly Ala Thr Gly Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile 460 465 470 475	1925
aca agc att ttg atg agg gca aag ccc cac gaa gtg aag atg atg atg Thr Ser Ile Leu Met Arg Ala Lys Pro His Glu Val Lys Met Met Met 480 485 490	1973
att gat ccg aaa atg gtc gag ctc aat gtc tac aac ggg att ccg cat Ile Asp Pro Lys Met Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His 495 500 505	2021
ttg ctc gct ccc gtc gtg aca gac ccg aaa aaa gca tcg cag gct ttg Leu Leu Ala Pro Val Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu 510 515 520	2069
aag aaa gtc gtc aac gaa atg gag cgg cgc tac gaa ttg ttt tct cac Lys Lys Val Val Asn Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His 525 530 535	2117

10295.204.ST25.txt

acg gga acg aga aat atc gaa ggg tat aac gac tat att aaa cgg atg Thr Gly Thr Arg Asn Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met 540 545 550 555	2165
aat gcc gca gaa gaa gca aag cag ccg gag ctt cca tac atc att gtg Asn Ala Ala Glu Glu Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val 560 565 570	2213
att gtg gac gag ctt gcc gac ctg atg atg gtc gct tcc tct gat gtt Ile Val Asp Glu Leu Ala Asp Leu Met Met Val Ala Ser Ser Asp Val 575 580 585	2261
gaa gac tcg atc aca agg ctt tcg caa atg gcc agg gcg gcg ggc atc Glu Asp Ser Ile Thr Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile 590 595 600	2309
cac ctg atc att gcg acg cag agg cct tcg gtc gat gtt atc aca ggg His Leu Ile Ile Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly 605 610 615	2357
gtc att aaa gcc aac att ccg tca agg atc gct ttc agc gta tcg tct Val Ile Lys Ala Asn Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser 620 625 630 635	2405
cag acc gac tcc agg acg att ctt gat atg gga ggc gct gaa aaa ctt Gln Thr Asp Ser Arg Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu 640 645 650	2453
ctc ggc aga ggg gac atg ctg ttt ctc cct gtc ggc gcc aat aaa ccg Leu Gly Arg Gly Asp Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro 655 660 665	2501
ctc cgc gtt caa ggt gcc ttt ctg tca gac gaa gaa gtt gaa aaa gtt Leu Arg Val Gln Gly Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val 670 675 680	2549
gtc gat cac gtc atc agc cag caa aaa gcc caa tac caa gaa gaa atg Val Asp His Val Ile Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met 685 690 695	2597
att cca gaa gag acg cag gaa acg gtc agc gaa gtg aca gac gac ctt Ile Pro Glu Glu Thr Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu 700 705 710 715	2645
tat gac gaa gcg gtc gca ctt gtg gtc agc atg cag acg gct tct gta Tyr Asp Glu Ala Val Ala Leu Val Val Ser Met Gln Thr Ala Ser Val 720 725 730	2693
tcc atg ctg caa agg aga ttc cgc atc ggc tat aca aga gcg gcg ccg Ser Met Leu Gln Arg Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg 735 740 745	2741
ctt atc gat gcc atg gaa gag ccg gga atc gtc ggc cca tat gaa gga Leu Ile Asp Ala Met Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly 750 755 760	2789
tca aaa ccc cgt gaa gtt ctc ttg tca aaa gag caa tac gaa gaa ctc Ser Lys Pro Arg Glu Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu 765 770 775	2837
tct tct tgagaagaga gttcttggtt aacataattt cattatgtaa actaaaaaac Ser Ser 780	2893
atctatttat ttatttgaca aaacatgata tagttatcct caattaaaga taatttgaat	2953
ctgatctgtc agacggagggg aaaacatgtc gataaaagct gacaatcaac gggtatgttt	3013

10295.204.ST25.txt

aaaggtgatt gatcggataa aagatgatat tcaaaatggg gtcttttgcg aaaatgaacg 3073
 gctcccgagt gaatttgagc tgtcaaagat gcttggtgtg agcagaacgg ctttgcgtga 3133
 ggcgcttaga atactggaag aagaaaacgt catcatcaga aggcatggag tcggacattt 3193
 tgtaaagtcc agaccgttat ttctatcagg tattgagcag ctgaacagcg tcacaaaaat 3253
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 cactgaagaa gatatgctcc ggtttcaata tgc 3346

<210> 67
 <211> 781
 <212> PRT
 <213> Bacillus licheniformis

<400> 67

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 20 25 30

Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val Ala Gly Gln Thr Phe
 35 40 45

Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp Phe Ile Leu Cys Leu
 50 55 60

Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe Trp Lys Lys Lys Thr
 65 70 75 80

Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu Tyr Cys Ile Ile Ala
 85 90 95

Ser Met Leu Leu Leu Ser His Val Gln Leu Phe Gln His Leu Thr Glu
 100 105 110

Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln Asn Thr Trp Glu Leu
 115 120 125

Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser Pro Asp Leu Gly Gly
 130 135 140

Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser Tyr Phe Leu Phe Ala
 145 150 155 160

Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu Ile Leu Ile Gly Leu
 165 170 175

Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr Leu Ile Lys Trp Met
 180 185 190

10295.204.ST25.txt

Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp Gln Ala Phe Leu Ala
195 200 205

Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys Lys Lys Ser Gly Lys
210 215 220

Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser Glu Glu Pro Val Gln
225 230 235 240

Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln Ser Glu Pro Ile Ile
245 250 255

Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu Val Gln Ala Tyr Glu
260 265 270

Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu Pro Glu Ile Gly Glu
275 280 285

Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr Phe Thr Glu Leu Glu
290 295 300

Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu Leu Asp Asp Pro Lys
305 310 315 320

His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile Tyr Asp Asn Ala Arg
325 330 335

Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val Lys Ala Lys Val Thr
340 345 350

Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr Glu Val Tyr Pro Asp
355 360 365

Val Gly Val Lys Val Ser Lys Ile Val Asn Leu Ser Asp Asp Leu Ala
370 375 380

Leu Ala Leu Ala Ala Lys Asp Ile Arg Ile Glu Ala Pro Ile Pro Gly
385 390 395 400

Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala Glu Val Ala Met Val
405 410 415

Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn Asp Arg Pro Asp Ala
420 425 430

Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser Gly Glu Ala Val Leu
435 440 445

Ala Glu Leu Asn Lys Met Pro His Leu Leu Val Ala Gly Ala Thr Gly
450 455 460

10295.204.ST25.txt

Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile Thr Ser Ile Leu Met
 465 470 475 480
 Arg Ala Lys Pro His Glu Val Lys Met Met Met Ile Asp Pro Lys Met
 485 490 495
 Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His Leu Leu Ala Pro Val
 500 505 510
 Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu Lys Lys Val Val Asn
 515 520 525
 Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His Thr Gly Thr Arg Asn
 530 535 540
 Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met Asn Ala Ala Glu Glu
 545 550 555 560
 Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val Ile Val Asp Glu Leu
 565 570 575
 Ala Asp Leu Met Met Val Ala Ser Ser Asp Val Glu Asp Ser Ile Thr
 580 585 590
 Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile His Leu Ile Ile Ala
 595 600 605
 Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Val Ile Lys Ala Asn
 610 615 620
 Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser Gln Thr Asp Ser Arg
 625 630 635 640
 Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp
 645 650 655
 Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro Leu Arg Val Gln Gly
 660 665 670
 Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val Val Asp His Val Ile
 675 680 685
 Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met Ile Pro Glu Glu Thr
 690 695 700
 Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu Tyr Asp Glu Ala Val
 705 710 715 720
 Ala Leu Val Val Ser Met Gln Thr Ala Ser Val Ser Met Leu Gln Arg
 725 730 735

10295.204.ST25.txt

Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg Leu Ile Asp Ala Met
 740 745 750

Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly Ser Lys Pro Arg Glu
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Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu Ser Ser
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<210> 68
 <211> 1045
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
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 tttattatcg ttccggcagt caatactgtc atcggctatt tggtcatcaa gtttcagctg 180
 attccgccga tcgcatacgc tgttccgtgg acaacgccag ggccgttgat tccgtttctc 240
 gggaccggag gaaactggct tgcgctcggc gtcggctttc tctgcctcgc catttcaacg 300
 atgatttatc tgccgtttgt gatggctgcc aacaagactg tgaatacggg cagggagcat 360
 tccgcggaaa acaggaagga atcataactt tagacggggc gccttttacg ggcgcccgtc 420
 tttttttaaa aaaagtcatg cggctctctt ttctctcata caatctatta aaatcaaaag 480
 cacgtctggg aggaagatac atg cgg aag ccc aca atc aaa gag ctc atc ttt 533
 Met Arg Lys Pro Thr Ile Lys Glu Leu Ile Phe
 1 5 10
 caa cat atg aag gac cat ctg tcg atc tat tta ttt gtt tct gtg ctg 581
 Gln His Met Lys Asp His Leu Ser Ile Tyr Leu Phe Val Ser Val Leu
 15 20 25
 ttc tta atg ggt gtg att ttc ggc gcg gtc atc gtc aac agc atg acg 629
 Phe Leu Met Gly Val Ile Phe Gly Ala Val Ile Val Asn Ser Met Thr
 30 35 40
 atc ggt caa aaa gaa gat ttg ttc tac tat ttg aat caa ttt ttt gga 677
 Ile Gly Gln Lys Glu Asp Leu Phe Tyr Tyr Leu Asn Gln Phe Phe Gly
 45 50 55
 cag ctt tcc gaa gga aaa gca gcc agc tca aag gaa atg ttt ttg cag 725
 Gln Leu Ser Glu Gly Lys Ala Ala Ser Ser Lys Glu Met Phe Leu Gln
 60 65 70 75
 agc ttt ctt cat aat atg aaa tat tta ggc tta atg tgg att ctc ggg 773
 Ser Phe Leu His Asn Met Lys Tyr Leu Gly Leu Met Trp Ile Leu Gly
 80 85 90
 ata tcc atc atc ggt ctg ccc gtc att ttt atc atg gtc ttc tta aaa 821
 Ile Ser Ile Ile Gly Leu Pro Val Ile Phe Ile Met Val Phe Leu Lys
 95 100 105

10295.204.ST25.txt

ggg atc gtc gtc gga ttt aca gtc ggc ttt ttg gtc aat caa atg gga 869
 Gly Ile Val Val Gly Phe Thr Val Gly Phe Leu Val Asn Gln Met Gly
 110 115 120
 atc aac ggc ttt ttc ctg tct ttt gtc tcc gtg ctc ccg caa aat att 917
 Ile Asn Gly Phe Phe Leu Ser Phe Val Ser Val Leu Pro Gln Asn Ile
 125 130 135
 ctg ctg atc ccg gcg tac ttg atc atg ggc acc tgc gcc atc gcc ttt 965
 Leu Leu Ile Pro Ala Tyr Leu Ile Met Gly Thr Cys Ala Ile Ala Phe
 140 145 150 155
 tcg atg agg ctc atc cgc cag ctt ttt gta aac gca gcc ttc aga agc 1013
 Ser Met Arg Leu Ile Arg Gln Leu Phe Val Asn Ala Ala Phe Arg Ser
 160 165 170
 acc tgt cca tgt gtt gtg ccg cgg gta gcc ga 1045
 Thr Cys Pro Cys Val Val Pro Arg Val Ala
 175 180

<210> 69
 <211> 181
 <212> PRT
 <213> Bacillus licheniformis

<400> 69

Met Arg Lys Pro Thr Ile Lys Glu Leu Ile Phe Gln His Met Lys Asp
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His Leu Ser Ile Tyr Leu Phe Val Ser Val Leu Phe Leu Met Gly Val
 20 25 30

Ile Phe Gly Ala Val Ile Val Asn Ser Met Thr Ile Gly Gln Lys Glu
 35 40 45

Asp Leu Phe Tyr Tyr Leu Asn Gln Phe Phe Gly Gln Leu Ser Glu Gly
 50 55 60

Lys Ala Ala Ser Ser Lys Glu Met Phe Leu Gln Ser Phe Leu His Asn
 65 70 75 80

Met Lys Tyr Leu Gly Leu Met Trp Ile Leu Gly Ile Ser Ile Ile Gly
 85 90 95

Leu Pro Val Ile Phe Ile Met Val Phe Leu Lys Gly Ile Val Val Gly
 100 105 110

Phe Thr Val Gly Phe Leu Val Asn Gln Met Gly Ile Asn Gly Phe Phe
 115 120 125

Leu Ser Phe Val Ser Val Leu Pro Gln Asn Ile Leu Leu Ile Pro Ala
 130 135 140

Tyr Leu Ile Met Gly Thr Cys Ala Ile Ala Phe Ser Met Arg Leu Ile
 145 150 155 160

Arg Gln Leu Phe Val Asn Ala Ala Phe Arg Ser Thr Cys Pro Cys Val
165 170 175

Val Pro Arg Val Ala
180

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<210> 70
<211> 1108
<212> DNA
<213> Bacillus licheniformis
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<221> CDS
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 tcc gcc gcc gac tca ggt ctt aaa aga gga gag aga agc gaa tct tgc 964
 Ser Ala Ala Asp Ser Gly Leu Lys Arg Gly Glu Arg Ser Glu Ser Cys
 140 145 150 155
 aga gct tca agg gaa aca gaa aaa gaa aac aga cgg gga aaa acc tcc 1012
 Arg Ala Ser Arg Glu Thr Glu Lys Glu Asn Arg Arg Gly Lys Thr Ser
 160 165 170
 tca aca atc gac ggg cgg ccg caa agt cgt att tat cta caa tac gca 1060
 Ser Thr Ile Asp Gly Arg Pro Gln Ser Arg Ile Tyr Leu Gln Tyr Ala
 175 180 185
 caa tac gga atc gta tct tcc cct ttt aaa agg tca ggc aga tcc ttt 1108
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 190 195 200

<210> 71
 <211> 203
 <212> PRT
 <213> Bacillus licheniformis

<400> 71

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 20 25 30

Arg Phe Tyr Phe Ile Arg Arg Ala His Ile Ala Ala Ser Ser Val Lys
 35 40 45

Ala Val Phe Ile Val Val Pro Gly Gly Ser Ser Thr Glu Gly Arg Asp
 50 55 60

Leu Trp Ala His Phe Gly Asn Gly Lys Pro Leu Leu Cys Ile Arg Ile
 65 70 75 80

Ala Gly Thr Glu Ser Ala Leu Ser Ala Phe Pro Pro Arg Pro Glu Ala
 85 90 95

Gly Asp Gln His Ser Phe Glu Arg Ser Ala Lys Phe Ser Arg Thr Gly
 100 105 110

Ala Ser Gly Ile Leu Ser Phe Ser Leu Gly Asn Pro His Cys Arg Ala
 115 120 125

Arg Asp Gly Leu Tyr Glu Tyr Ala Val Arg Ile Ser Ala Ala Asp Ser
 130 135 140

Gly Leu Lys Arg Gly Glu Arg Ser Glu Ser Cys Arg Ala Ser Arg Glu
 145 150 155 160

Thr Glu Lys Glu Asn Arg Arg Gly Lys Thr Ser Ser Thr Ile Asp Gly
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165

170

175

Arg Pro Gln Ser Arg Ile Tyr Leu Gln Tyr Ala Gln Tyr Gly Ile Val
 180 185 190

Ser Ser Pro Phe Lys Arg Ser Gly Arg Ser Phe
 195 200

<210> 72
 <211> 1152
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
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 Met Ser Lys
 1
 aaa gag aaa gag aag aat cgt act tcc aaa atc aca aag ttg caa caa 163
 Lys Glu Lys Glu Lys Asn Arg Thr Ser Lys Ile Thr Lys Leu Gln Gln
 5 10 15
 ttt ttt cgt aaa cgc tgg gta ttt ccg gcc atc tat ttg aca agt gcc 211
 Phe Phe Arg Lys Arg Trp Val Phe Pro Ala Ile Tyr Leu Thr Ser Ala
 20 25 30 35
 gtc gtt gta tta acc gcc gtt cta tgg tat caa tcg gct tct aac aac 259
 Val Val Val Leu Thr Ala Val Leu Trp Tyr Gln Ser Ala Ser Asn Asn
 40 45 50
 gat gta aaa gac cag ctt gca gac gat ggc aag aaa tca gcc tat gat 307
 Asp Val Lys Asp Gln Leu Ala Asp Asp Gly Lys Lys Ser Ala Tyr Asp
 55 60 65
 aac cgg gat gat gcg gta gaa gta ggc aaa cca gtc gaa aat gtc gca 355
 Asn Arg Asp Asp Ala Val Glu Val Gly Lys Pro Val Glu Asn Val Ala
 70 75 80
 atg ccg gtt gct gat tct gaa aat gtt tcc gtc gtt aaa aag ttt ttt 403
 Met Pro Val Ala Asp Ser Glu Asn Val Ser Val Val Lys Lys Phe Phe
 85 90 95
 gaa act gac gca act aaa gaa gag aaa gaa gca gca ctt gta aac tat 451
 Glu Thr Asp Ala Thr Lys Glu Glu Lys Glu Ala Ala Leu Val Asn Tyr
 100 105 110 115
 aat aac acg tac agc atg agc aaa ggt atc gac ttg gct gag aaa gac 499
 Asn Asn Thr Tyr Ser Met Ser Lys Gly Ile Asp Leu Ala Glu Lys Asp
 120 125 130
 gga aaa aca ttt gat gtt tcc gca tct cta agc ggt acg gtc atc aaa 547
 Gly Lys Thr Phe Asp Val Ser Ala Ser Leu Ser Gly Thr Val Ile Lys
 135 140 145
 gct gca aaa gac cct gta ctg ggc tac gtt gtt gaa gtt gaa cat gaa 595
 Ala Ala Lys Asp Pro Val Leu Gly Tyr Val Val Glu Val Glu His Glu
 150 155 160

10295.204.ST25.txt

gat ggt tta tca act gtg tat cag tct ctt tct gaa gta agc gtc aaa 643
 Asp Gly Leu Ser Thr Val Tyr Gln Ser Leu Ser Glu Val Ser Val Lys
 165 170 175
 caa ggt gac aag att gaa caa aat caa gtc atc gga aaa gca ggc aaa 691
 Gln Gly Asp Lys Ile Glu Gln Asn Gln Val Ile Gly Lys Ala Gly Lys
 180 185 190 195
 aac ctt tac aat gaa gaa ggc gga aac cat gtg cat ttt gaa atc cgc 739
 Asn Leu Tyr Asn Glu Glu Gly Gly Asn His Val His Phe Glu Ile Arg
 200 205 210
 aaa gac ggt gtt gcg cta aac ccg ctg aac ttc atg gac aag ccg gtc 787
 Lys Asp Gly Val Ala Leu Asn Pro Leu Asn Phe Met Asp Lys Pro Val
 215 220 225
 tcc agc att gaa aaa gca atg gag gaa caa gcg tct gaa gtg aaa gaa 835
 Ser Ser Ile Glu Lys Ala Met Glu Glu Gln Ala Ser Glu Val Lys Glu
 230 235 240
 cct gct cag cct tct gtt gaa gaa aag tca aaa aca gaa gac aaa gcg 883
 Pro Ala Gln Pro Ser Val Glu Glu Lys Ser Lys Thr Glu Asp Lys Ala
 245 250 255
 aaa gat caa aca gat gga aaa gac gac aaa acc aag cgg gaa gat tcg 931
 Lys Asp Gln Thr Asp Gly Lys Asp Asp Lys Thr Lys Arg Glu Asp Ser
 260 265 270 275
 tct gaa ggg tca gaa aat caa gac gga acc cag tct gac gat tca agc 979
 Ser Glu Gly Ser Glu Asn Gln Asp Gly Thr Gln Ser Asp Asp Ser Ser
 280 285 290
 cag tca taaggcagc ttccctcagg gcgcctatca aatgcgatag gcgccttttt 1035
 Gln Ser
 tggtacaatc aaaaaaaacc cgtatcaaat cggcggagcc agccgttttt aagtaagagg 1095
 cctctttaag gagtggaagg cattaggaag taagtagaac agcaaaccgc ctagtaa 1152

<210> 73
 <211> 293
 <212> PRT
 <213> Bacillus licheniformis

<400> 73

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20 25 30

Thr Ser Ala Val Val Val Leu Thr Ala Val Leu Trp Tyr Gln Ser Ala
35 40 45

Ser Asn Asn Asp Val Lys Asp Gln Leu Ala Asp Asp Gly Lys Lys Ser
50 55 60

Ala Tyr Asp Asn Arg Asp Asp Ala Val Glu Val Gly Lys Pro Val Glu
65 70 75 80

10295.204.ST25.txt

Asn Val Ala Met Pro Val Ala Asp Ser Glu Asn Val Ser Val Val Lys
 85 90 95

Lys Phe Phe Glu Thr Asp Ala Thr Lys Glu Glu Lys Glu Ala Ala Leu
 100 105 110

Val Asn Tyr Asn Asn Thr Tyr Ser Met Ser Lys Gly Ile Asp Leu Ala
 115 120 125

Glu Lys Asp Gly Lys Thr Phe Asp Val Ser Ala Ser Leu Ser Gly Thr
 130 135 140

Val Ile Lys Ala Ala Lys Asp Pro Val Leu Gly Tyr Val Val Glu Val
 145 150 155 160

Glu His Glu Asp Gly Leu Ser Thr Val Tyr Gln Ser Leu Ser Glu Val
 165 170 175

Ser Val Lys Gln Gly Asp Lys Ile Glu Gln Asn Gln Val Ile Gly Lys
 180 185 190

Ala Gly Lys Asn Leu Tyr Asn Glu Glu Gly Gly Asn His Val His Phe
 195 200 205

Glu Ile Arg Lys Asp Gly Val Ala Leu Asn Pro Leu Asn Phe Met Asp
 210 215 220

Lys Pro Val Ser Ser Ile Glu Lys Ala Met Glu Glu Gln Ala Ser Glu
 225 230 235 240

Val Lys Glu Pro Ala Gln Pro Ser Val Glu Glu Lys Ser Lys Thr Glu
 245 250 255

Asp Lys Ala Lys Asp Gln Thr Asp Gly Lys Asp Asp Lys Thr Lys Arg
 260 265 270

Glu Asp Ser Ser Glu Gly Ser Glu Asn Gln Asp Gly Thr Gln Ser Asp
 275 280 285

Asp Ser Ser Gln Ser
 290

<210> 74
 <211> 1747
 <212> DNA
 <213> Bacillus licheniformis

<220>
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 <222> (501)..(1244)

<400> 74
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60

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tcatccattt taggcgtggg cgcttccac cggtgaaag gcgtaaactg gggcaccgca	300
aagcggatgc tgatcacttg ggtcattacc cttcccattt cggcaaccat cgggtgcattt	360
gcctatttca tacttgattt attcttttaa tcagcacact cccgtccgaa tctaggacgg	420
gagttttcat gtttaaaaga aagccggcat aacaatagaa ataggaactg cactatttct	480
cggaagagg gaaacaagtt atg ctg cta ttt tat caa ttc ctt gtt tgg ctt	533
Met Leu Leu Phe Tyr Gln Phe Leu Val Trp Leu	
1 5 10	
att gtt ttg gcg ctg gct ctg tac gta gct gcc gtg tgg cgt ttt gaa	581
Ile Val Leu Ala Leu Ala Leu Tyr Val Ala Ala Val Trp Arg Phe Glu	
15 20 25	
aaa cag ctc gcc gaa aaa acg gtc gcc atc aga aaa acg tgg tac ctt	629
Lys Gln Leu Ala Glu Lys Thr Val Ala Ile Arg Lys Thr Trp Tyr Leu	
30 35 40	
ctt tat gtc atc ggc gcc gtg ata tat tgg acg cac gat ccg cag tca	677
Leu Tyr Val Ile Gly Ala Val Ile Tyr Trp Thr His Asp Pro Gln Ser	
45 50 55	
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Ile Phe Thr Asn Pro Leu His Tyr Leu Ile Val Ala Val Phe Phe Thr	
60 65 70 75	
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Leu Thr Asp Ala Phe Ile Phe Leu Asn Ala Tyr Phe Lys Lys Leu Gly	
80 85 90	
agc tct gaa ctc gcg aca gat aca aga atg ctt ctc gaa gaa aac aac	821
Ser Ser Glu Leu Ala Thr Asp Thr Arg Met Leu Leu Glu Glu Asn Asn	
95 100 105	
gac ctc ctc cac acg tat caa aac agg ctg aaa acg ttt caa tac cta	869
Asp Leu Leu His Thr Tyr Gln Asn Arg Leu Lys Thr Phe Gln Tyr Leu	
110 115 120	
ttg aaa aac gaa ccg atc cac atc tat tat gga aat ata gaa gcg tat	917
Leu Lys Asn Glu Pro Ile His Ile Tyr Tyr Gly Asn Ile Glu Ala Tyr	
125 130 135	
gca gaa ggc atc gaa aag ctc atc aaa cgg ttt gcc gaa aaa atg aat	965
Ala Glu Gly Ile Glu Lys Leu Ile Lys Arg Phe Ala Glu Lys Met Asn	
140 145 150 155	
ata tcc gct gca ctt tgc gaa tat aat tca gaa gaa agc aag gat cat	1013
Ile Ser Ala Ala Leu Cys Glu Tyr Asn Ser Glu Glu Ser Lys Asp His	
160 165 170	
ttg ctt gag cat atg gaa aac cgg ttc gat gtt caa gaa aag ctt gac	1061
Leu Leu Glu His Met Glu Asn Arg Phe Asp Val Gln Glu Lys Leu Asp	
175 180 185	
cgc aaa gac gtt tat tat gaa gaa aac gga aaa atg gtc ctc att cct	1109
Arg Lys Asp Val Tyr Tyr Glu Glu Asn Gly Lys Met Val Leu Ile Pro	
190 195 200	
ttt tcc atc cac gat ttt gac tat gtc atg aag tta acc tca gaa gac	1157

10295.204.ST25.txt

Phe Ser Ile His Asp Phe Asp Tyr Val Met Lys Leu Thr Ser Glu Asp
 205 210 215
 ctt gtc aca gaa ttt gat tat ctc ctg ttt act tct tta aca agc atc 1205
 Leu Val Thr Glu Phe Asp Tyr Leu Leu Phe Thr Ser Leu Thr Ser Ile
 220 225 230 235
 tat gat ctt ctg cta cca aac gaa gag gaa ggt gac gac tgatggagcc 1254
 Tyr Asp Leu Leu 240 Leu Pro Asn Glu Glu Gly Asp Asp 245
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<210> 75
 <211> 248
 <212> PRT
 <213> Bacillus licheniformis

<400> 75

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Lys Thr Val Ala Ile Arg Lys Thr Trp Tyr Leu Leu Tyr Val Ile Gly
 35 40 45

Ala Val Ile Tyr Trp Thr His Asp Pro Gln Ser Ile Phe Thr Asn Pro
 50 55 60

Leu His Tyr Leu Ile Val Ala Val Phe Phe Thr Leu Thr Asp Ala Phe
 65 70 75 80

Ile Phe Leu Asn Ala Tyr Phe Lys Lys Leu Gly Ser Ser Glu Leu Ala
 85 90 95

Thr Asp Thr Arg Met Leu Leu Glu Glu Asn Asn Asp Leu Leu His Thr
 100 105 110

Tyr Gln Asn Arg Leu Lys Thr Phe Gln Tyr Leu Leu Lys Asn Glu Pro
 115 120 125

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10295.204.ST25.txt

caa tta caa act tta cgt caa tat act cag tta tat ggt tgg gag att Gln Leu Gln Thr Leu Arg Gln Tyr Thr Gln Leu Tyr Gly Trp Glu Ile 30 35 40	629
gca gag gaa tat gta gat gag gga ata agt gga aag aac att agc ggt Ala Glu Glu Tyr Val Asp Glu Gly Ile Ser Gly Lys Asn Ile Ser Gly 45 50 55	677
cgc cct gca atg caa aaa ctt att tca gat gtt gaa aag gat aaa ttt Arg Pro Ala Met Gln Lys Leu Ile Ser Asp Val Glu Lys Asp Lys Phe 60 65 70 75	725
caa gct gtt ctt gtt tgg aag atc tca cgc cta tca cga aat atg tta Gln Ala Val Leu Val Trp Lys Ile Ser Arg Leu Ser Arg Asn Met Leu 80 85 90	773
gat act ctc act cta tta gac aaa ttc gaa gat tat gga gta aag ttc Asp Thr Leu Thr Leu Leu Asp Lys Phe Glu Asp Tyr Gly Val Lys Phe 95 100 105	821
atc tct tac tct gaa aac ttt gat aca ggc agt cca att ggt cgt tta Ile Ser Tyr Ser Glu Asn Phe Asp Thr Gly Ser Pro Ile Gly Arg Leu 110 115 120	869
gtt gtt caa cta atg gct tcc att gca gaa atg gag cgt aat acg tta Val Val Gln Leu Met Ala Ser Ile Ala Glu Met Glu Arg Asn Thr Leu 125 130 135	917
tct gag aac gtt aag ctc gga atg aaa cag aga gca tta gaa ggt tca Ser Glu Asn Val Lys Leu Gly Met Lys Gln Arg Ala Leu Glu Gly Ser 140 145 150 155	965
tgg aat gga ggc gtt gta ttt ggc tac gat aca att gaa aaa gag ctt Trp Asn Gly Gly Val Val Phe Gly Tyr Asp Thr Ile Glu Lys Glu Leu 160 165 170	1013
gtg atc aac aaa aag gaa gct gag att gta caa caa atc tat caa cta Val Ile Asn Lys Lys Glu Ala Glu Ile Val Gln Gln Ile Tyr Gln Leu 175 180 185	1061
tat gcc aat ggt aaa ggc tta aag tca atc gca aac tac tta aat aaa Tyr Ala Asn Gly Lys Gly Leu Lys Ser Ile Ala Asn Tyr Leu Asn Lys 190 195 200	1109
gca ggt tac aga act aaa cgg aat tgt tat ttt tcg ata aac ggt gta Ala Gly Tyr Arg Thr Lys Arg Asn Cys Tyr Phe Ser Ile Asn Gly Val 205 210 215	1157
gct caa atc tta gac aat gtt atc tat aac ggg aag atc agt tgg tta Ala Gln Ile Leu Asp Asn Val Ile Tyr Asn Gly Lys Ile Ser Trp Leu 220 225 230 235	1205
aaa gtt gaa aat tgg gat aca aaa cgg agg aga ggg aaa aat cca aat Lys Val Glu Asn Trp Asp Thr Lys Arg Arg Arg Gly Lys Asn Pro Asn 240 245 250	1253
cct atc ctt gta gaa gga cag cat gaa gcc att att tcc gat gaa tta Pro Ile Leu Val Glu Gly Gln His Glu Ala Ile Ile Ser Asp Glu Leu 255 260 265	1301
tgg agt atg gta caa gca agg cgg aaa agt aaa tca ttt aaa caa agg Trp Ser Met Val Gln Ala Arg Arg Lys Ser Lys Ser Phe Lys Gln Arg 270 275 280	1349
caa tct aat gaa cca ttt tta ctt agc agt ctt tta cgt tgc ccc gat Gln Ser Asn Glu Pro Phe Leu Leu Ser Ser Leu Leu Arg Cys Pro Asp 285 290 295	1397

10295.204.ST25.txt

tgt ggt caa ggt atg gtt cct gcc att aca aca aat aaa cga aag gat 1445
 Cys Gly Gln Gly Met Val Pro Ala Ile Thr Thr Asn Lys Arg Lys Asp
 300 305 310 315

gga aca aag aag aaa tat cgt tat tat gtt tgc tct aac ttt cat aac 1493
 Gly Thr Lys Lys Lys Tyr Arg Tyr Tyr Val Cys Ser Asn Phe His Asn
 320 325 330

aaa ggt tca tct gca tgt aga gca aat tca ata aaa gca tat gat gca 1541
 Lys Gly Ser Ser Ala Cys Arg Ala Asn Ser Ile Lys Ala Tyr Asp Ala
 335 340 345

gaa tac gaa gta att aat aag att gag aag atc ctt tcc aac caa aat 1589
 Glu Tyr Glu Val Ile Asn Lys Ile Glu Lys Ile Leu Ser Asn Gln Asn
 350 355 360

cag tta ttc tct aaa ctt caa tct ata aat act act tcg att gaa tct 1637
 Gln Leu Phe Ser Lys Leu Gln Ser Ile Asn Thr Thr Ser Ile Glu Ser
 365 370 375

tta aac caa ctc aat agt gaa ttg aaa caa tta gaa aat cgc cta tca 1685
 Leu Asn Gln Leu Asn Ser Glu Leu Lys Gln Leu Glu Asn Arg Leu Ser
 380 385 390 395

gaa ata caa gag tac aga atc gtt act tgg aag cat ttg agc aaa aga 1733
 Glu Ile Gln Glu Tyr Arg Ile Val Thr Trp Lys His Leu Ser Lys Arg
 400 405 410

cct tac caa tagcaatctt gcaagaacga ttacagcatg tctctaaaga 1782
 Pro Tyr Gln

aaaagcagag ttagaacaaa ggcacaatga atcactgggc aattaagctc gaacgatgca 1842
 aaagtaataa aaccagaact gattcaaaag ctttagaaaa aattccttta gtctataaac 1902
 atcatcaaga gaaagcaaaa cagttactca acttttgctt ataaattaca gtaagcatca 1962
 atgggtcatc acgattgtcg atcaattgaa ctcgactttg actttcagaa gtcattatt 2020

<210> 77
 <211> 414
 <212> PRT
 <213> Bacillus licheniformis

<400> 77

Met His Glu Ile Lys Arg Val Ala Ile Tyr Cys Arg Val Ser Thr Glu
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Glu Gln Ala Thr Glu Gly Tyr Ser Ile Ser Ala Gln Leu Gln Thr Leu
 20 25 30

Arg Gln Tyr Thr Gln Leu Tyr Gly Trp Glu Ile Ala Glu Glu Tyr Val
 35 40 45

Asp Glu Gly Ile Ser Gly Lys Asn Ile Ser Gly Arg Pro Ala Met Gln
 50 55 60

Lys Leu Ile Ser Asp Val Glu Lys Asp Lys Phe Gln Ala Val Leu Val
 65 70 75 80

10295.204.ST25.txt

Trp Lys Ile Ser Arg Leu Ser Arg Asn Met Leu Asp Thr Leu Thr Leu
 85 90 95

Leu Asp Lys Phe Glu Asp Tyr Gly Val Lys Phe Ile Ser Tyr Ser Glu
 100 105 110

Asn Phe Asp Thr Gly Ser Pro Ile Gly Arg Leu Val Val Gln Leu Met
 115 120 125

Ala Ser Ile Ala Glu Met Glu Arg Asn Thr Leu Ser Glu Asn Val Lys
 130 135 140

Leu Gly Met Lys Gln Arg Ala Leu Glu Gly Ser Trp Asn Gly Gly Val
 145 150 155 160

Val Phe Gly Tyr Asp Thr Ile Glu Lys Glu Leu Val Ile Asn Lys Lys
 165 170 175

Glu Ala Glu Ile Val Gln Gln Ile Tyr Gln Leu Tyr Ala Asn Gly Lys
 180 185 190

Gly Leu Lys Ser Ile Ala Asn Tyr Leu Asn Lys Ala Gly Tyr Arg Thr
 195 200 205

Lys Arg Asn Cys Tyr Phe Ser Ile Asn Gly Val Ala Gln Ile Leu Asp
 210 215 220

Asn Val Ile Tyr Asn Gly Lys Ile Ser Trp Leu Lys Val Glu Asn Trp
 225 230 235 240

Asp Thr Lys Arg Arg Arg Gly Lys Asn Pro Asn Pro Ile Leu Val Glu
 245 250 255

Gly Gln His Glu Ala Ile Ile Ser Asp Glu Leu Trp Ser Met Val Gln
 260 265 270

Ala Arg Arg Lys Ser Lys Ser Phe Lys Gln Arg Gln Ser Asn Glu Pro
 275 280 285

Phe Leu Leu Ser Ser Leu Leu Arg Cys Pro Asp Cys Gly Gln Gly Met
 290 295 300

Val Pro Ala Ile Thr Thr Asn Lys Arg Lys Asp Gly Thr Lys Lys Lys
 305 310 315 320

Tyr Arg Tyr Tyr Val Cys Ser Asn Phe His Asn Lys Gly Ser Ser Ala
 325 330 335

Cys Arg Ala Asn Ser Ile Lys Ala Tyr Asp Ala Glu Tyr Glu Val Ile
 340 345 350

gcc att gcc tac aaa ggc cag ttt gaa ccc gca aac caa atc aaa ccg 821

10295.204.ST25.txt

Ala Ile Ala Tyr Lys Gly Gln Phe Glu Pro Ala Asn Gln Ile Lys Pro
 90 95 100

gtt atc agc cag gtg ttt act gaa gag ttc caa ttt gcg gcc ctc cag 869
 Val Ile Ser Gln Val Phe Thr Glu Glu Phe Gln Phe Ala Ala Leu Gln
 105 110 115 120

aat tgg tat gaa tcc aag ttc ggc gat ccc ctc gca ttc ttt cag ccg 917
 Asn Trp Tyr Glu Ser Lys Phe Gly Asp Pro Leu Ala Phe Phe Gln Pro
 125 130 135

aaa ggc gcc aaa ccg tcc ggc cag gtc gag gtg aat cag gat ctc gct 965
 Lys Gly Ala Lys Pro Ser Gly Gln Val Glu Val Asn Gln Asp Leu Ala
 140 145 150

gta cct gcc gta gga aag gtt cag gag aaa ttc tca ggg cag ggc att 1013
 Val Pro Ala Val Gly Lys Val Gln Glu Lys Phe Ser Gly Gln Gly Ile
 155 160 165

aag gta gaa aca gaa gac gaa acg atc cgc agc atg aag gaa ggc tat 1061
 Lys Val Glu Thr Glu Asp Glu Thr Ile Arg Ser Met Lys Glu Gly Tyr
 170 175 180

gtc att gaa gtg gac aaa aat ccg gaa aca ggc ctg acg gtg gtc ttg 1109
 Val Ile Glu Val Asp Lys Asn Pro Glu Thr Gly Leu Thr Val Val Leu
 185 190 195 200

cag cat gcg gac aac agc tat acc tac tac ggc cag ctg aaa aaa gcg 1157
 Gln His Ala Asp Asn Ser Tyr Thr Tyr Tyr Gly Gln Leu Lys Lys Ala
 205 210 215

gat gtc gct tta tac gat tat ata gat aaa gga acg aag ctc gga acg 1205
 Asp Val Ala Leu Tyr Asp Tyr Ile Asp Lys Gly Thr Lys Leu Gly Thr
 220 225 230

att gag cag gat aaa aat caa aaa ggc atc tat tac ttt gcg atc aaa 1253
 Ile Glu Gln Asp Lys Asn Gln Lys Gly Ile Tyr Tyr Phe Ala Ile Lys
 235 240 245

caa gga gag gaa ttt gtt gat ccg ata cag gtg atc aca ttt gag 1298
 Gln Gly Glu Glu Phe Val Asp Pro Ile Gln Val Ile Thr Phe Glu
 250 255 260

taaatggacg gagctcttca ccaagcttca cattcatccg ctgctgtggc ttgtcatggc 1358

gatcgggtatc atgacaggac atattaaagg cgcgtgtttt gtttaatgca cccaggaag 1417

<210> 79

<211> 263

<212> PRT

<213> Bacillus licheniformis

<400> 79

Met Ser His Arg Ala Asp Glu Ile Arg Lys Arg Met Ala Arg Lys Arg
 1 5 10 15

Lys Arg Lys Thr Pro Asp Lys Gln Pro Phe Ser Ser Asp Gly Lys Lys
 20 25 30

Arg Pro Leu Lys Pro Pro Ala Trp Thr Ala Phe Ser Glu Asp Glu Lys
 35 40 45

Gly Gly Asp Phe Pro Pro Pro Glu Gly Ser Ser Leu Leu Ile Asn Gly
 Page 110

10295.204.ST25.txt

50

55

60

Lys His Pro Leu Val Lys Ala Asp Ala Leu Ile Leu Lys Cys Leu Leu
 65 70 75 80

Ser Ala Cys Leu Val Leu Val Ser Ala Ile Ala Tyr Lys Gly Gln Phe
 85 90 95

Glu Pro Ala Asn Gln Ile Lys Pro Val Ile Ser Gln Val Phe Thr Glu
 100 105 110

Glu Phe Gln Phe Ala Ala Leu Gln Asn Trp Tyr Glu Ser Lys Phe Gly
 115 120 125

Asp Pro Leu Ala Phe Phe Gln Pro Lys Gly Ala Lys Pro Ser Gly Gln
 130 135 140

Val Glu Val Asn Gln Asp Leu Ala Val Pro Ala Val Gly Lys Val Gln
 145 150 155 160

Glu Lys Phe Ser Gly Gln Gly Ile Lys Val Glu Thr Glu Asp Glu Thr
 165 170 175

Ile Arg Ser Met Lys Glu Gly Tyr Val Ile Glu Val Asp Lys Asn Pro
 180 185 190

Glu Thr Gly Leu Thr Val Val Leu Gln His Ala Asp Asn Ser Tyr Thr
 195 200 205

Tyr Tyr Gly Gln Leu Lys Lys Ala Asp Val Ala Leu Tyr Asp Tyr Ile
 210 215 220

Asp Lys Gly Thr Lys Leu Gly Thr Ile Glu Gln Asp Lys Asn Gln Lys
 225 230 235 240

Gly Ile Tyr Tyr Phe Ala Ile Lys Gln Gly Glu Glu Phe Val Asp Pro
 245 250 255

Ile Gln Val Ile Thr Phe Glu
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<210> 80

<211> 1468

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (982)..(1428)

<400> 80

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10295.204.ST25.txt

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tgaagctgta cataaatcgt ttcctgacct tgatgtccaa accgtcggcg gttctgaaac	180
catcgtggag atccaatatc cgaaaaggga tctgtcgcgc gtgcttttca tcgccgtctg	240
gctgctcttg ttcgtcgggt ccggccttgc cgtcatgaac tttcatgaag atgtcagcat	300
gagggaagt cacatcctgc tttacgaaat ggtgacgggc aaggtgaacc gctatccata	360
ccttttgcag gttccgtaca gcatcgggtc tggcctcggc atgatcttgt tttttaatca	420
tttatttaaa aaacggttta acgaggagcc cagccccctg gaggtcgaga tgtttaataa	480
tcagcttgat ttggaccatt atgtggccat gcacgaaaac aaagaaacga caaaggatat	540
tcgatcatcat tagcgtgata tttatcatct ttctcggact cgcaggaggg gttgctgttg	600
gatccggctt tgtcgttttt cttaccgtgc ttggcattat cccgaggctg actcagctga	660
cgaaaacaaa aggatttatc caggcgtatg aatgggctgt cattttaggc gcggttttcg	720
gaggatggga atcgtgaac atgtcccgt ttttttatc caaatggctg cttgttccga	780
tcggcctttt tgcgggcgtt ttcattggaa tgcttgacgc ggcgctaaca gaagtcttga	840
acgtgctgcc gatactggcg aaacgcacgc ggatgggaga ccggattttg ataçtttta	900
tggccattgt tttcggcaag attctcggat cgatgttcca atggctcatt tttgttcatt	960
tgtcataaaa ggaggattat g atg tca agt ttg aaa gat aat tat caa tcg	1011
Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser	10
1 5	
aaa gtt aaa gcg tat cag cct tca ccg cct tat gtc ctg aac tgt atc	1059
Lys Val Lys Ala Tyr Gln Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile	25
15 20	
aag gca ttt ctc gtc ggt ggt ctg att tgt acg atc ggc cag gct ttc	1107
Lys Ala Phe Leu Val Gly Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe	40
30 35	
cag aat ttt tat atg gct gtg ttc cat ttt gat gaa aaa acg gcc ggg	1155
Gln Asn Phe Tyr Met Ala Val Phe His Phe Asp Glu Lys Thr Ala Gly	55
45 50	
aac ccg acg gtt gcc acg ctg atc ctg atc tcc gct ctg tta aca ggc	1203
Asn Pro Thr Val Ala Thr Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly	70
60 65	
ctt ggc gtc tac gac aga atc gga cag ttt gcc ggc gct ggt tct gcc	1251
Leu Gly Val Tyr Asp Arg Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala	90
75 80	
gtt ccg gtt aca ggg ttt gcc aac agt atg acg agc gca gcg ctg gag	1299
Val Pro Val Thr Gly Phe Ala Asn Ser Met Thr Ser Ala Ala Leu Glu	105
95 100	
cat aaa agc gaa agc tac gtc ctc ggc gta tgg aca aac atg ttc aag	1347
His Lys Ser Glu Ser Tyr Val Leu Gly Val Trp Thr Asn Met Phe Lys	120
110 115	
ctt gcg gga aac gtc atc gtg ttc ggt gtt gtg gcc gct tat att gtg	1395
Leu Ala Gly Asn Val Ile Val Phe Gly Val Val Ala Ala Tyr Ile Val	135
125 130	
ggg atg atc cgc ttt gcc ttt gac aag ctg ttt taggaggaaa acatcatgaa	1448
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10295.204.ST25.txt

140

- 145

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1468

<210> 81
 <211> 149
 <212> PRT
 <213> Bacillus licheniformis

<400> 81

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Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile Lys Ala Phe Leu Val Gly
 20 25 30

Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe Gln Asn Phe Tyr Met Ala
 35 40 45

Val Phe His Phe Asp Glu Lys Thr Ala Gly Asn Pro Thr Val Ala Thr
 50 55 60

Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly Leu Gly Val Tyr Asp Arg
 65 70 75 80

Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala Val Pro Val Thr Gly Phe
 85 90 95

Ala Asn Ser Met Thr Ser Ala Ala Leu Glu His Lys Ser Glu Ser Tyr
 100 105 110

Val Leu Gly Val Trp Thr Asn Met Phe Lys Leu Ala Gly Asn Val Ile
 115 120 125

Val Phe Gly Val Val Ala Ala Tyr Ile Val Gly Met Ile Arg Phe Ala
 130 135 140

Phe Asp Lys Leu Phe
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<210> 82
 <211> 1453
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (504)..(950)

<400> 82
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 tggatccggc tttgtcgctt ttcttaccgt gcttggcatt atcccagggc tgactcagct 180

gacgaaaaca aaaggatttta tccaggcgta tgaatgggct gtcatttttag gcgcgggtttt	240
cggaggatgg gaatcgctga acatgtcccg ctttttttta tccaaatggc tgcttggtcc	300
gatcggcctt tttgcgggcg ttttcattgg aatgcttgca gcggcgctaa cagaagtctt	360
gaacgtgctg ccgatactgg cgaaacgcat cgggatggga gaccggattt tgatactttt	420
aatggccatt gttttcggca agattctcgg atcgatgttc caatggctca tttttgttca	480
tttgtcataa aaggaggatt atg atg tca agt ttg aaa gat aat tat caa tcg	533
Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser	10
1 5	
aaa gtt aaa gcg tat cag cct tca ccg cct tat gtc ctg aac tgt atc	581
Lys Val Lys Ala Tyr Gln Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile	25
15 20	
aag gca ttt ctc gtc ggt ggt ctg att tgt acg atc ggc cag gct ttc	629
Lys Ala Phe Leu Val Gly Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe	40
30 35	
cag aat ttt tat atg gct gtg ttc cat ttt gat gaa aaa acg gcc ggg	677
Gln Asn Phe Tyr Met Ala Val Phe His Phe Asp Glu Lys Thr Ala Gly	55
45 50	
aac ccg acg gtt gcc acg ctg atc ctg atc tcc gct ctg tta aca ggc	725
Asn Pro Thr Val Ala Thr Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly	60 70
60 65 70	
ctt ggc gtc tac gac aga atc gga cag ttt gcc ggc gct ggt tct gcc	773
Leu Gly Val Tyr Asp Arg Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala	75 80 85 90
75 80 85 90	
gtt ccg gtt aca ggg ttt gcc aac agt atg acg agc gca gcg ctg gag	821
Val Pro Val Thr Gly Phe Ala Asn Ser Met Thr Ser Ala Ala Leu Glu	95 100 105
95 100 105	
cat aaa agc gaa agc tac gtc ctc ggc gta tgg aca aac atg ttc aag	869
His Lys Ser Glu Ser Tyr Val Leu Gly Val Trp Thr Asn Met Phe Lys	110 115 120
110 115 120	
ctt gcg gga aac gtc atc gtg ttc ggt gtt gtg gcc gct tat att gtg	917
Leu Ala Gly Asn Val Ile Val Phe Gly Val Val Ala Ala Tyr Ile Val	125 130 135
125 130 135	
ggg atg atc cgc ttt gcc ttt gac aag ctg ttt taggaggaaa acatcatgaa	970
Gly Met Ile Arg Phe Ala Phe Asp Lys Leu Phe	140 145
140 145	
attaacagga aaacaaacat gggaattcga gaaccgcgtg tttgttaact caagcggaac	1030
agcggtcggt cccaaagaaa aagaagggtc tcttgacac ttatttgaca aaagctatga	1090
tgaaatgcac tgcaaccaga aaaactggga aatggcagag cgcaagctga tggaggatgc	1150
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gttgattgac ggggggtttcg caaagcgcgc cctagcggca accagcagcc ataatgctac	1390
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10295.204.ST25.txt

<210> 83
 <211> 149
 <212> PRT
 <213> Bacillus licheniformis

<400> 83

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 20 25 30

Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe Gln Asn Phe Tyr Met Ala
 35 40 45

Val Phe His Phe Asp Glu Lys Thr Ala Gly Asn Pro Thr Val Ala Thr
 50 55 60

Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly Leu Gly Val Tyr Asp Arg
 65 70 75 80

Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala Val Pro Val Thr Gly Phe
 85 90 95

Ala Asn Ser Met Thr Ser Ala Ala Leu Glu His Lys Ser Glu Ser Tyr
 100 105 110

Val Leu Gly Val Trp Thr Asn Met Phe Lys Leu Ala Gly Asn Val Ile
 115 120 125

Val Phe Gly Val Val Ala Ala Tyr Ile Val Gly Met Ile Arg Phe Ala
 130 135 140

Phe Asp Lys Leu Phe
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<210> 84
 <211> 2020
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1517)

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 catttctcgt cggtggtctg atttgtacga tcggccaggc tttccagaat ttttatatgg 180
 ctgtgttcca ttttgatgaa aaaacggccg ggaacccgac gggtgccacg ctgatcctga 240

10295.204.ST25.txt

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aaagcgaaaag ctacgtcctc ggcgtatgga caaacatggt caagcttgcg ggaaacgtca	420
tcgtgttcgg tggtgtggcc gcttatattg tggggatgat ccgctttgcc tttgacaagc	480
tgtttttagga ggaaaacatc atg aaa tta aca gga aaa caa aca tgg gaa ttc	533
Met Lys Leu Thr Gly Lys Gln Thr Trp Glu Phe	10
gag aac ccg ctg ttt gtt aac tca agc gga aca gcg gtc ggt ccc aaa	581
Glu Asn Pro Leu Phe Val Asn Ser Ser Gly Thr Ala Val Gly Pro Lys	25
gaa aaa gaa ggt cct ctt gga cac tta ttt gac aaa agc tat gat gaa	629
Glu Lys Glu Gly Pro Leu Gly His Leu Phe Asp Lys Ser Tyr Asp Glu	40
atg cac tgc aac cag aaa aac tgg gaa atg gca gag cgc aag ctg atg	677
Met His Cys Asn Gln Lys Asn Trp Glu Met Ala Glu Arg Lys Leu Met	55
gag gat gcg gtt cag tcc gcg tta tca aaa caa aat ctt aaa aag gaa	725
Glu Asp Ala Val Gln Ser Ala Leu Ser Lys Gln Asn Leu Lys Lys Glu	75
gac atc gat atc ttt ttg gct ggc gat ctg ctc aac caa aac gtg aca	773
Asp Ile Asp Ile Phe Leu Ala Gly Asp Leu Leu Asn Gln Asn Val Thr	90
gcc aac tat gtg gcg cgg cat ttg aaa att cct ttt ctc tgc tta ttt	821
Ala Asn Tyr Val Ala Arg His Leu Lys Ile Pro Phe Leu Cys Leu Phe	105
gga gca tgc tcg aca tca atg gaa tcg atc gcg atc agt tcg gcg ttg	869
Gly Ala Cys Ser Thr Ser Met Glu Ser Ile Ala Ile Ser Ser Ala Leu	120
att gac ggg ggt ttc gca aag cgc gcc cta gcg gca acc agc agc cat	917
Ile Asp Gly Gly Phe Ala Lys Arg Ala Leu Ala Ala Thr Ser Ser His	135
aat gct acg gca gaa agg cag ttc cgc tac ccg acg gaa tac ggg ggg	965
Asn Ala Thr Ala Glu Arg Gln Phe Arg Tyr Pro Thr Glu Tyr Gly Gly	155
caa aaa ccg gga acc gcg act tcg aca gtg acc gga agc gga gcg gtc	1013
Gln Lys Pro Gly Thr Ala Thr Ser Thr Val Thr Gly Ser Gly Ala Val	170
gtc ctc agc cag cag ccc ggc gga att aaa att aca agc gca act gtc	1061
Val Leu Ser Gln Gln Pro Gly Gly Ile Lys Ile Thr Ser Ala Thr Val	185
gga agg gtt atc gac ttg ggg att acc gat tcg caa gat atg ggg tcg	1109
Gly Arg Val Ile Asp Leu Gly Ile Thr Asp Ser Gln Asp Met Gly Ser	200
gcg atg gca ccc gct gct gcg gat acg atc aag cag cat ttg gag gat	1157
Ala Met Ala Pro Ala Ala Ala Asp Thr Ile Lys Gln His Leu Glu Asp	215
ctg gga cgc acc cct gat gat tac gat ctg atc tta acc ggc gac ctt	1205
Leu Gly Arg Thr Pro Asp Asp Tyr Asp Leu Ile Leu Thr Gly Asp Leu	235

10295.204.ST25.txt

tca ggc gtc ggc agc ccg att ttg aag gat ctg tta aaa gag gaa gga 1253
 Ser Gly Val Gly Ser Pro Ile Leu Lys Asp Leu Leu Lys Glu Glu Gly 250

atc aat gtc ggg aca aaa cat aat gac tgc ggg ctg atg atc tat acg 1301
 Ile Asn Val Gly Thr Lys His Asn Asp Cys Gly Leu Met Ile Tyr Thr 255 260 265

cct gac cag caa gtt ttt gca ggt gga agc gga tgc gct tgt tcc gcg 1349
 Pro Asp Gln Gln Val Phe Ala Gly Gly Ser Gly Cys Ala Cys Ser Ala 270 275 280

gtc gtc acc ttt gcc cat att ttc aaa gaa att gaa gcg gga agg ctg 1397
 Val Val Thr Phe Ala His Ile Phe Lys Glu Ile Glu Ala Gly Arg Leu 285 290 295

aac aga gtg ctt gtt gtc gcg aca ggc gcc ctt tta agc ccg acg atc 1445
 Asn Arg Val Leu Val Val Ala Thr Gly Ala Leu Leu Ser Pro Thr Ile 300 305 310 315

atc cag caa aaa gaa tcg ata cca tgc att gcc cat ggc gtc gta ttt 1493
 Ile Gln Gln Lys Glu Ser Ile Pro Cys Ile Ala His Gly Val Val Phe 320 325 330

gaa cgg gcc gaa agg ggg aac gct taagatggag tatgtcattg cttttattgc 1547
 Glu Arg Ala Glu Arg Gly Asn Ala 335

aggcgggctg atttgcgtca tcggacagct cttgcttgat atcttcaaaa tgacgccggc 1607
 tcatgtcatg tcaacttttg tcgtatctgg agcgatcctt gacggattcg gcatttacga 1667
 ccgtttttatc gaatttgccg gtgccggggc tacagtcccg attgtcagct tcggccactc 1727
 tcttttgcac ggcgcgatgc accaggctga gaaacatggc tttatcggaa tcggcatggg 1787
 gatatttgaa ctgacatctg ccggtatatc tgccgctatc ttgttcgctt ttcttggtgc 1847
 cgtgattttt aaaccgaaag gataaaggaa aatgccagca aaacgcaagg tcattttggg 1907
 cacagacggc gatatatatc ctgcaaaagc aatcgaatat gcagcaagaa aaacggggtg 1967
 ccgctgcatt tcccaatcgg cggggaatcc gagcgtaaaa acaggaccgg agc 2020

<210> 85
 <211> 339
 <212> PRT
 <213> Bacillus licheniformis

<400> 85
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 Val Asn Ser Ser Gly Thr Ala Val Gly Pro Lys Glu Lys Glu Gly Pro
 20 25 30
 Leu Gly His Leu Phe Asp Lys Ser Tyr Asp Glu Met His Cys Asn Gln
 35 40 45
 Lys Asn Trp Glu Met Ala Glu Arg Lys Leu Met Glu Asp Ala Val Gln
 50 55 60

10295.204.ST25.txt

Ser Ala Leu Ser Lys Gln Asn Leu Lys Lys Glu Asp Ile Asp Ile Phe
65 70 75 80

Leu Ala Gly Asp Leu Leu Asn Gln Asn Val Thr Ala Asn Tyr Val Ala
85 90 95

Arg His Leu Lys Ile Pro Phe Leu Cys Leu Phe Gly Ala Cys Ser Thr
100 105 110

Ser Met Glu Ser Ile Ala Ile Ser Ser Ala Leu Ile Asp Gly Gly Phe
115 120 125

Ala Lys Arg Ala Leu Ala Ala Thr Ser Ser His Asn Ala Thr Ala Glu
130 135 140

Arg Gln Phe Arg Tyr Pro Thr Glu Tyr Gly Gly Gln Lys Pro Gly Thr
145 150 155 160

Ala Thr Ser Thr Val Thr Gly Ser Gly Ala Val Val Leu Ser Gln Gln
165 170 175

Pro Gly Gly Ile Lys Ile Thr Ser Ala Thr Val Gly Arg Val Ile Asp
180 185 190

Leu Gly Ile Thr Asp Ser Gln Asp Met Gly Ser Ala Met Ala Pro Ala
195 200 205

Ala Ala Asp Thr Ile Lys Gln His Leu Glu Asp Leu Gly Arg Thr Pro
210 215 220

Asp Asp Tyr Asp Leu Ile Leu Thr Gly Asp Leu Ser Gly Val Gly Ser
225 230 235 240

Pro Ile Leu Lys Asp Leu Leu Lys Glu Glu Gly Ile Asn Val Gly Thr
245 250 255

Lys His Asn Asp Cys Gly Leu Met Ile Tyr Thr Pro Asp Gln Gln Val
260 265 270

Phe Ala Gly Gly Ser Gly Cys Ala Cys Ser Ala Val Val Thr Phe Ala
275 280 285

His Ile Phe Lys Glu Ile Glu Ala Gly Arg Leu Asn Arg Val Leu Val
290 295 300

Val Ala Thr Gly Ala Leu Leu Ser Pro Thr Ile Ile Gln Gln Lys Glu
305 310 315 320

Ser Ile Pro Cys Ile Ala His Gly Val Val Phe Glu Arg Ala Glu Arg
325 330 335

Gly Asn Ala

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cgtcatgttt gatgattccg gacttcaagg tgaaggcccc ggagagacag ctatgaaata	180
tgttagcgatg catcccata ttcgaggtgct cggagtcatc gccgtcgctt caaaaactca	240
ttatgcagag tgagacgag tcgatgtatc aatcgatgca gaaggcgaac tgacagagta	300
cggcgtcgat aaacacgggg tcaaagagtt cgatgtcaaa cgaatgaatg gtgatacagt	360
ctattgcctt gaccagctgg atgtttccgat cattgtcggg atcgggtgata tcggtaagat	420
gaacagaaaa gacgatgtgg aaaaagggtt gccgattaca atgaaagcgg tcgagctcat	480
tttagaaagg agcgggtatc attg agt gct caa aag' caa gag aag acg aac gta Met Ser Ala Gln Lys Gln Glu Lys Thr Asn Val 1 5 10	533
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atg gga gaa agc ttt gac ctt ggc gta cgg aag gtc ttt att ctc gga Met Gly Glu Ser Phe Asp Leu Gly Val Arg Lys Val Phe Ile Leu Gly 30 35 40	629
cat gaa gtt cag ctt tat tat gtc aac gga ttg tgc gac aca caa tac His Glu Val Gln Leu Tyr Tyr Val Asn Gly Leu Cys Asp Thr Gln Tyr 45 50 55	677
atc att cac ctg tta aga gaa ctg gtg cat ctg aat gat aaa gaa aaa Ile Ile His Leu Leu Arg Glu Leu Val His Leu Asn Asp Lys Glu Lys 60 65 70 75	725
gaa tcg ggc gag gtc gaa gac atc gtc gaa aac agg ctt ttg aac cag Glu Ser Gly Glu Val Glu Asp Ile Val Glu Asn Arg Leu Leu Asn Gln 80 85 90	773
cag gtt tca aaa gcg gaa acg ctt gat gaa gct gtc gac caa gtg ttg Gln Val Ser Lys Ala Glu Thr Leu Asp Glu Ala Val Asp Gln Val Leu 95 100 105	821
tca gga ctg gtt gcc atc atc gtc gaa gat gcg ggc ttt gct ttt atc Ser Gly Leu Val Ala Ile Ile Val Glu Asp Ala Gly Phe Ala Phe Ile 110 115 120	869
atc gat gtc aga agc tac ccg ggc aga acg ccg gaa gaa cct gat aca Ile Asp Val Arg Ser Tyr Pro Gly Arg Thr Pro Glu Glu Pro Asp Thr 125 130 135	917
gaa aaa gtc gta cgc ggt gca agg gac gga ctc gtc gag aac atc atc	965

10295.204.ST25.txt

Glu Lys Val Val Arg Gly Ala Arg Asp Gly Leu Val Glu Asn Ile Ile
 140 145 150 155
 gtc aac aca gcc ctg att aga cgc cgg atc aga gat gag cgc ttg cgc 1013
 Val Asn Thr Ala Leu Ile Arg Arg Arg Ile Arg Asp Glu Arg Leu Arg
 160 165 170
 tac aaa atg ctt cat atc ggt gaa cgc tct aaa aca gac atc tgc ctc 1061
 Tyr Lys Met Leu His Ile Gly Glu Arg Ser Lys Thr Asp Ile Cys Leu
 175 180 185
 tgc tat ttg gaa gac gtt gca gat ccc gat ctt gtt gaa gta tta aaa 1109
 Cys Tyr Leu Glu Asp Val Ala Asp Pro Asp Leu Val Glu Val Leu Lys
 190 195 200
 aaa gaa att gaa gat gtg aag atc gac ggg ctg ccg atg tcg gat aaa 1157
 Lys Glu Ile Glu Asp Val Lys Ile Asp Gly Leu Pro Met Ser Asp Lys
 205 210 215
 tcg gta gag gaa ttc ctg gtc ggc caa ggc tac aat ccg ttt ccg ctt 1205
 Ser Val Glu Glu Phe Leu Val Gly Gln Gly Tyr Asn Pro Phe Pro Leu
 220 225 230 235
 gtc agg ttt acg gaa agg gca gac gta gcc gca agc cat att tta gag 1253
 Val Arg Phe Thr Glu Arg Ala Asp Val Ala Ala Ser His Ile Leu Glu
 240 245 250
 ggg cat gtc atc gtg atc gtc gat acg tcg cca agc gtc atc atc aca 1301
 Gly His Val Ile Val Ile Val Asp Thr Ser Pro Ser Val Ile Ile Thr
 255 260 265
 ccg acc act ttg ttt cac cat gtt cag cat gct gag gaa tac aga cag 1349
 Pro Thr Thr Leu Phe His His Val Gln His Ala Glu Glu Tyr Arg Gln
 270 275 280
 acg ccg gct gtt ggg acg ttt tta agg tgg gtg ccg ttt ttc ggt att 1397
 Thr Pro Ala Val Gly Thr Phe Leu Arg Trp Val Arg Phe Phe Gly Ile
 285 290 295
 ttg gcc tcc acc ttt ttg ctg ccg ctt tgg ctg ctg ttt gtc att cat 1445
 Leu Ala Ser Thr Phe Leu Leu Pro Leu Trp Leu Leu Phe Val Ile His
 300 305 310 315
 ccg tcg ctc ttg cct gat aat tta tcg ttt atc ggg ttg aat aaa gac 1493
 Pro Ser Leu Leu Pro Asp Asn Leu Ser Phe Ile Gly Leu Asn Lys Asp
 320 325 330
 acc cat att ccg att atc atg cag att ttc ctg gcg gat ctc ggc gtc 1541
 Thr His Ile Pro Ile Ile Met Gln Ile Phe Leu Ala Asp Leu Gly Val
 335 340 345
 gaa ttt tta aga atg gcc gcc att cat acg ccg acg gcg ctt tcg act 1589
 Glu Phe Leu Arg Met Ala Ala Ile His Thr Pro Thr Ala Leu Ser Thr
 350 355 360
 gca atg ggc ctg atc gcc gct gta ttg atc ggc gat atc gcg atc aat 1637
 Ala Met Gly Leu Ile Ala Ala Val Leu Ile Gly Asp Ile Ala Ile Asn
 365 370 375
 gtc ggc ttg ttt tct ccc gaa gtc att tta tac gtt tcc ctc tcg gca 1685
 Val Gly Leu Phe Ser Pro Glu Val Ile Leu Tyr Val Ser Leu Ser Ala
 380 385 390 395
 atc gga gcc tac acg aca cca agc tac gag ctg agc ctg gcg aat aaa 1733
 Ile Gly Ala Tyr Thr Pro Ser Tyr Glu Leu Ser Leu Ala Asn Lys
 400 405 410
 atg gtg aag ctg ttt atg ctg ata ttg gtg gcg ctt ttt aaa gtg gag 1781

10295.204.ST25.txt

Met Val Lys Leu Phe Met Leu Ile Leu Val Ala Leu Phe Lys Val Glu
 415 420 425

gga ttt gtc atc gga tta acg atc tta act ata gtg atg act tcg atc 1829
 Gly Phe Val Ile Gly Leu Thr Ile Leu Thr Ile Val Met Thr Ser Ile
 430 435 440

agg tca ttg cga acg cct tac tta tgg cct ctc ctc ccg ttc aat gga 1877
 Arg Ser Leu Arg Thr Pro Tyr Leu Trp Pro Leu Leu Pro Phe Asn Gly
 445 450 455

aaa gcg ttt tgg cat gtt ctc gtg cgc acg tcc gtt cca ggg gga aaa 1925
 Lys Ala Phe Trp His Val Leu Val Arg Thr Ser Val Pro Gly Gly Lys
 460 465 470 475

gtc agg ccg agc atc gtt cat ccg aga aac cgc tcc aga cag ccg 1970
 Val Arg Pro Ser Ile Val His Pro Arg Asn Arg Ser Arg Gln Pro
 480 485 490

tgaagccggc attcgaagag gcttttcccc ggggaaaagc ctctttttca ataatcgaat 2030
 tccgggtcttt gagtaccgat gcctctgtat tcattggcag agatcgcgac tgcccggagg 2090
 ctgcagatgt tgttctgtct tctgatcgga tagacgacat acagcatttc gcggccgtac 2150
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 gccggagctg taataatctg cccctcataa ggctcataaa ttctctgttc ataatgcgca 2270
 gccggctgat aaggggcgta tacatcttca ggtgcatagc cgggagcggg ggtgtagggg 2330
 taacgatttg gatacatatg ataacctctt tcccacttcg ttttttggtt ttcattctta 2390
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 ttttattgaa tggacgttgt gta 2473

<210> 87
 <211> 490
 <212> PRT
 <213> Bacillus licheniformis

<400> 87

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Lys Asn Glu Ala Tyr Phe Lys Lys Arg Val Gly Met Gly Glu Ser Phe
 20 25 30

Asp Leu Gly Val Arg Lys Val Phe Ile Leu Gly His Glu Val Gln Leu
 35 40 45

Tyr Tyr Val Asn Gly Leu Cys Asp Thr Gln Tyr Ile Ile His Leu Leu
 50 55 60

Arg Glu Leu Val His Leu Asn Asp Lys Glu Lys Glu Ser Gly Glu Val
 65 70 75 80

Glu Asp Ile Val Glu Asn Arg Leu Leu Asn Gln Gln Val Ser Lys Ala
 85 90 95

10295.204.ST25.txt

Glu Thr Leu Asp Glu Ala Val Asp Gln Val Leu Ser Gly Leu Val Ala
 100 105 110
 Ile Ile Val Glu Asp Ala Gly Phe Ala Phe Ile Ile Asp Val Arg Ser
 115 120 125
 Tyr Pro Gly Arg Thr Pro Glu Glu Pro Asp Thr Glu Lys Val Val Arg
 130 135 140
 Gly Ala Arg Asp Gly Leu Val Glu Asn Ile Ile Val Asn Thr Ala Leu
 145 150 155 160
 Ile Arg Arg Arg Ile Arg Asp Glu Arg Leu Arg Tyr Lys Met Leu His
 165 170 175
 Ile Gly Glu Arg Ser Lys Thr Asp Ile Cys Leu Cys Tyr Leu Glu Asp
 180 185 190
 Val Ala Asp Pro Asp Leu Val Glu Val Leu Lys Lys Glu Ile Glu Asp
 195 200 205
 Val Lys Ile Asp Gly Leu Pro Met Ser Asp Lys Ser Val Glu Glu Phe
 210 215 220
 Leu Val Gly Gln Gly Tyr Asn Pro Phe Pro Leu Val Arg Phe Thr Glu
 225 230 235 240
 Arg Ala Asp Val Ala Ala Ser His Ile Leu Glu Gly His Val Ile Val
 245 250 255
 Ile Val Asp Thr Ser Pro Ser Val Ile Ile Thr Pro Thr Thr Leu Phe
 260 265 270
 His His Val Gln His Ala Glu Glu Tyr Arg Gln Thr Pro Ala Val Gly
 275 280 285
 Thr Phe Leu Arg Trp Val Arg Phe Phe Gly Ile Leu Ala Ser Thr Phe
 290 295 300
 Leu Leu Pro Leu Trp Leu Leu Phe Val Ile His Pro Ser Leu Leu Pro
 305 310 315 320
 Asp Asn Leu Ser Phe Ile Gly Leu Asn Lys Asp Thr His Ile Pro Ile
 325 330 335
 Ile Met Gln Ile Phe Leu Ala Asp Leu Gly Val Glu Phe Leu Arg Met
 340 345 350
 Ala Ala Ile His Thr Pro Thr Ala Leu Ser Thr Ala Met Gly Leu Ile
 355 360 365

10295.204.ST25.txt

Ala Ala Val Leu Ile Gly Asp Ile Ala Ile Asn Val Gly Leu Phe Ser
 370 375 380

Pro Glu Val Ile Leu Tyr Val Ser Leu Ser Ala Ile Gly Ala Tyr Thr
 385 390 395 400

Thr Pro Ser Tyr Glu Leu Ser Leu Ala Asn Lys Met Val Lys Leu Phe
 405 410 415

Met Leu Ile Leu Val Ala Leu Phe Lys Val Glu Gly Phe Val Ile Gly
 420 425 430

Leu Thr Ile Leu Thr Ile Val Met Thr Ser Ile Arg Ser Leu Arg Thr
 435 440 445

Pro Tyr Leu Trp Pro Leu Leu Pro Phe Asn Gly Lys Ala Phe Trp His
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Val Leu Val Arg Thr Ser Val Pro Gly Gly Lys Val Arg Pro Ser Ile
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Val His Pro Arg Asn Arg Ser Arg Gln Pro
 485 490

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 <212> DNA
 <213> Bacillus licheniformis

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 cagccgcttt acgagctgtc tgtcacagca aagccgaaga acattccgca gacgatcgag 180
 gttgatattt ccagtctcga agtcaatgat gttctaaccg tcggcgatat tccgaccaa 240
 ggcgattatt catacaacca tgagcctgat gaagttggtg catccattct tcctcctcaa 300
 aagcaggaag aaacagaagc cgaatcagct gctcaagacg ttgaggaacc agaaaaaggc 360
 actgaagagg aaaaagaaga ataaatacgt aagacgtaat ccgcccgcgg ttacgtcttt 420
 tgtgctagaa tgaggggaaa ttaggatgct cccctcagt atgctgaggc agggttttgc 480
 ttaagggagg atatagaata atg ctt gtg ttt gca gga ttg ggc aat ccg ggt 533
 Met Leu Val Phe Ala Gly Leu Gly Asn Pro Gly
 1 5 10
 aaa aca tat gaa aat acg aga cac aat gta ggt ttt atg acg att gac 581
 Lys Thr Tyr Glu Asn Thr Arg His Asn Val Gly Phe Met Thr Ile Asp
 15 20 25

10295.204.ST25.txt

gag ctc tcg aaa gag tgg aac att ccg ctt gat aaa aca aag ttc aac 629
 Glu Leu Ser Lys Glu Trp Asn Ile Pro Leu Asp Lys Thr Lys Phe Asn
 30 35 40

gga caa tac gga atc ggg ttt gtt tcc ggc aaa aag gtt cta ctt gtt 677
 Gly Gln Tyr Gly Ile Gly Phe Val Ser Gly Lys Lys Val Leu Leu Val
 45 50 55

aag ccg ctt aca tat atg aat tta tcg gga gaa tgt ttg agg ccg ctt 725
 Lys Pro Leu Thr Tyr Met Asn Leu Ser Gly Glu Cys Leu Arg Pro Leu
 60 65 70 75

ttg gac tat tac gag atc cct gtt gac aat ttg aaa gtg att tac gat 773
 Leu Asp Tyr Tyr Glu Ile Pro Val Asp Asn Leu Lys Val Ile Tyr Asp
 80 85 90

gat ttg gat ctt ccg acc gga aga atc cgt ctg agg acg aaa gga agc 821
 Asp Leu Asp Leu Pro Thr Gly Arg Ile Arg Leu Arg Thr Lys Gly Ser
 95 100 105

gca gga ggc cat aac ggc atc aaa tcg acg att cag cat ctg gga aca 869
 Ala Gly Gly His Asn Gly Ile Lys Ser Thr Ile Gln His Leu Gly Thr
 110 115 120

agt gag ttt aac cgg atc aga atc gga ata ggc cgt ccg gta aac ggc 917
 Ser Glu Phe Asn Arg Ile Arg Ile Gly Ile Gly Arg Pro Val Asn Gly
 125 130 135

atg aaa gtc gtc gat tat gtg ctt ggc gct ttt aca gat gaa gaa gag 965
 Met Lys Val Val Asp Tyr Val Leu Gly Ala Phe Thr Asp Glu Glu Glu
 140 145 150 155

ccg gcg ata aaa gag gcc gtc aga caa tcg gcc aag gcc tgt gaa gct 1013
 Pro Ala Ile Lys Glu Ala Val Arg Gln Ser Ala Lys Ala Cys Glu Ala
 160 165 170

tct ttg gaa aaa cct ttt tta gaa gtc atg aat gaa ttt aac gca aag 1061
 Ser Leu Glu Lys Pro Phe Leu Glu Val Met Asn Glu Phe Asn Ala Lys
 175 180 185

gta taaggcaaaa gggaacggaa catactagtc ttaaaaagac tcggtatgga 1114
 Val

gggttccttta tggctttaca ttattattgc cggcattgcg gcgttaaagt cggaagtctt 1174

gaccattctt atgtaaacag tgaacagtta ggctttaacc acttaacaaa tgatgaaaga 1234

aacgatatga tttcttatat ggataatggg gatttacacg tgaagacgat atgtgaagat 1294

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atagctttgg tgtagagact agaccaaagc atttttctat ttgaggaaga gaggaggggc 1414

tcatttgaac aatattcaat cctatataac aaaaagcgat gattttaaat ccatcgtaa 1474

cggcttgaac gaagggctga aggaacagct gcttgcgggg ctctccggat ctgcccggtc 1534

gttatttaca gccgctctta caaaagaaac gag 1567

<210> 89
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 <212> PRT
 <213> Bacillus licheniformis
 <400> 89

10295.204.ST25.txt

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 1 5 10 15

Thr Arg His Asn Val Gly Phe Met Thr Ile Asp Glu Leu Ser Lys Glu
 20 25 30

Trp Asn Ile Pro Leu Asp Lys Thr Lys Phe Asn Gly Gln Tyr Gly Ile
 35 40 45

Gly Phe Val Ser Gly Lys Lys Val Leu Leu Val Lys Pro Leu Thr Tyr
 50 55 60

Met Asn Leu Ser Gly Glu Cys Leu Arg Pro Leu Leu Asp Tyr Tyr Glu
 65 70 75 80

Ile Pro Val Asp Asn Leu Lys Val Ile Tyr Asp Asp Leu Asp Leu Pro
 85 90 95

Thr Gly Arg Ile Arg Leu Arg Thr Lys Gly Ser Ala Gly Gly His Asn
 100 105 110

Gly Ile Lys Ser Thr Ile Gln His Leu Gly Thr Ser Glu Phe Asn Arg
 115 120 125

Ile Arg Ile Gly Ile Gly Arg Pro Val Asn Gly Met Lys Val Val Asp
 130 135 140

Tyr Val Leu Gly Ala Phe Thr Asp Glu Glu Glu Pro Ala Ile Lys Glu
 145 150 155 160

Ala Val Arg Gln Ser Ala Lys Ala Cys Glu Ala Ser Leu Glu Lys Pro
 165 170 175

Phe Leu Glu Val Met Asn Glu Phe Asn Ala Lys Val
 180 185

<210> 90
 <211> 2097
 <212> DNA
 <213> Bacillus licheniformis

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 gtccgccttt caaaagccgg tcattttgct ggcagggggg cttgaccgag gaaatgaatt 180
 tgatgaacta aagccgcata tgtcttttgt aaaagcgggtg atcacttttcg gcgagaccgc 240
 gccgaagttt gagaagctgg ccgaagaaat gggaatacaa caggttaaac gtgtcgataa 300

10295.204.ST25.txt

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tgtaaacgcc gtgcatatgc ttaaataagg gcttgtctcg taaagatagc cctaagaatt	480
agagcttggg gtgttcggct ttg caa aca aaa aaa acg tca ccg gat ttt ttg	533
Leu Gln Thr Lys Lys Thr Ser Pro Asp Phe Leu	10
1	
ctg gtt atc att acg cta ttg ctt tta aca atc gga ctg att atg gta	581
Leu Val Ile Ile Thr Leu Leu Leu Thr Ile Gly Leu Ile Met Val	25
15	
tac agc gcc agt gca gta tgg gcg act tac aaa tac gac gac tcc ttt	629
Tyr Ser Ala Ser Ala Val Trp Ala Thr Tyr Lys Tyr Asp Asp Ser Phe	40
30	
35	
ttc ttt gcg aaa cgg cag ctt ttg ttt gcc ggc atc ggg gtc atc gcc	677
Phe Phe Ala Lys Arg Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala	55
45	
50	
atg ttt ttc atc atg aac gtc gac tac tgg acg tgg agg act tat gcg	725
Met Phe Phe Ile Met Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala	75
60	
65	
70	
aaa ata ctg atc att gta tgt ttc ttt ctg ctc atc atc gtc ctg gtt	773
Lys Ile Leu Ile Ile Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val	90
80	
85	
ccc ggg atc ggc atg gaa cgg aac ggg tcg agg agc tgg atc gga gtc	821
Pro Gly Ile Gly Met Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val	105
95	
100	
ggc gct ttc agc att cag ccg tcc gag ttt atg aaa ctc gcg atg atc	869
Gly Ala Phe Ser Ile Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile	120
110	
115	
gca ttt ttg gcc aag ttt tta tct gaa aag caa aag aat att acg tcg	917
Ala Phe Leu Ala Lys Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser	135
125	
130	
135	
ttt aga aaa ggc ttt gtg ccg gcg ctg ggc att gtc ttt tca gct ttt	965
Phe Arg Lys Gly Phe Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe	155
140	
145	
150	
ctg atc atc atg atg cag cct gac ctc gga aca gga acc gtg atg gtc	1013
Leu Ile Ile Met Met Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val	170
160	
165	
ggc aca tgc atc att atg atc ttt gtc gcg ggg gcg aga att tcg cac	1061
Gly Thr Cys Ile Ile Met Ile Phe Val Ala Gly Ala Arg Ile Ser His	185
175	
180	
ttc gtt ttt ctc ggc ctg atc gga ctg agc ggt ttt gtc ggc ctt gtg	1109
Phe Val Phe Leu Gly Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val	200
190	
195	
ctg tcg gcg ccg tac ccg atc aaa agg atc act tca tac ttg aac cct	1157
Leu Ser Ala Pro Tyr Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro	215
205	
210	
215	
tgg gag gac cct tta gga agc ggc ttt caa atc att cag tct ctt tat	1205
Trp Glu Asp Pro Leu Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr	235
220	
225	
230	
235	
gcg gtg ggg ccc ggc ggg ctg ttc ggc ctc ggc ctc ggc cag agc agg	1253

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10295.204.ST25.txt

35

40

45

Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala Met Phe Phe Ile Met
 50 55 60

Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala Lys Ile Leu Ile Ile
 65 70 75 80

Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val Pro Gly Ile Gly Met
 85 90 95

Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val Gly Ala Phe Ser Ile
 100 105 110

Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile Ala Phe Leu Ala Lys
 115 120 125

Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser Phe Arg Lys Gly Phe
 130 135 140

Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe Leu Ile Ile Met Met
 145 150 155 160

Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val Gly Thr Cys Ile Ile
 165 170 175

Met Ile Phe Val Ala Gly Ala Arg Ile Ser His Phe Val Phe Leu Gly
 180 185 190

Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val Leu Ser Ala Pro Tyr
 195 200 205

Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro Trp Glu Asp Pro Leu
 210 215 220

Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr Ala Val Gly Pro Gly
 225 230 235 240

Gly Leu Phe Gly Leu Gly Leu Gly Gln Ser Arg Gln Lys Phe Phe Tyr
 245 250 255

Leu Pro Glu Pro Gln Thr Asp Phe Ile Phe Ala Ile Leu Ser Glu Glu
 260 265 270

Leu Gly Phe Ile Gly Gly Ser Leu Ile Leu Leu Leu Phe Ser Val Leu
 275 280 285

Leu Trp Arg Gly Ile Arg Ile Ala Leu Gly Ala Pro Asp Leu Tyr Gly
 290 295 300

Ser Phe Val Ala Val Gly Val Ile Ser Met Ile Ala Ile Gln Val Met
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10295.204.ST25.txt
315

305

310

320

Ile Asn Ile Gly Val Val Thr Gly Leu Ile Pro Val Thr Gly Ile Thr
325 330 335

Leu Pro Phe Leu Ser Tyr Gly Gly Ser Ser Leu Thr Leu Met Leu Met
340 345 350

Ala Val Gly Val Leu Leu Asn Val Ser Arg Tyr Ser Arg Tyr
355 360 365

<210> 92
<211> 1882
<212> DNA
<213> Bacillus licheniformis

<220>
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<222> (501)..(1397)

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aaaagaaatc gttgatgtta agcggggccga acggctcggc gtactggggc agacggacct 180
tgagatcaat gagcaggacg gtcagattac cgctcttata atcccttctg ttaaattggt 240
cggactagga agaaaacagg ggaatgacat taagggtgccc tggctcgcaa ttcaaaaaat 300
cggctcggat atgatcattt tggatgttcc ggaaagcagc gtgacaaaag aggagtaagc 360
aagggtgga aa cccgcccgtc ccatgggggc gggctttttg tttttctgga tttcaattca 420
ccgctatttc ctttttgtca tatgatgaaa ttagcttatg aattagatcc ttgtcaaaaa 480
agaagggtgaa tgtagagcc atg tta acc gga ttg acg att gca atc atc ggc 533
Met Leu Thr Gly Leu Thr Ile Ala Ile Ile Gly
1 5 10

ggc gat gca agg cag ctc gag atc atc cgc aag ctg acg gaa cag gat 581
Gly Asp Ala Arg Gln Leu Glu Ile Ile Arg Lys Leu Thr Glu Gln Asp
15 20 25

gca aag gtc ttt tta atc ggt ttt gat cag ctt gat cac ggg ttt acc 629
Ala Lys Val Phe Leu Ile Gly Phe Asp Gln Leu Asp His Gly Phe Thr
30 35 40

gga gct aca aaa cta aag ctg aac gaa ctt gat ttt ggc aca ata gac 677
Gly Ala Thr Lys Leu Lys Leu Asn Glu Leu Asp Phe Gly Thr Ile Asp
45 50 55

agc att att ctg cct gta tcg ggc aca tcg atg gaa gga acg gtt gcg 725
Ser Ile Ile Leu Pro Val Ser Gly Thr Ser Met Glu Gly Thr Val Ala
60 65 70 75

act gtt ttt tcc aat gaa aaa gtg gtg tta aaa cag gaa cat tta gaa 773
Thr Val Phe Ser Asn Glu Lys Val Val Leu Lys Gln Glu His Leu Glu
80 85 90

aaa acc aag ccg cac tgc gcg att tat tca ggg att tca aac caa tat 821
Lys Thr Lys Pro His Cys Ala Ile Tyr Ser Gly Ile Ser Asn Gln Tyr
Page 129

10295.204.ST25.txt

95	100	105	
tta gac ggc atg gcc aaa ggg gcg aac cgt cgt ctt atc aag ctc ttt Leu Asp Gly Met Ala Lys Gly Ala Asn Arg Arg Leu Ile Lys Leu Phe 110 115 120			869
gaa aga gac gat att gcg att tac aac tcg ata cct aca gtc gaa ggt Glu Arg Asp Asp Ile Ala Ile Tyr Asn Ser Ile Pro Thr Val Glu Gly 125 130 135			917
gcc att atg atg gcc ata cag cat aca gac ttt acg att cac ggc tcg Ala Ile Met Met Ala Ile Gln His Thr Asp Phe Thr Ile His Gly Ser 140 145 150 155			965
aat gta atg gtt ctc ggg ctg ggg cgg acg gga atg agc atc agc cgg Asn Val Met Val Leu Gly Leu Gly Arg Thr Gly Met Ser Ile Ser Arg 160 165 170			1013
acg ttc tcg gcg ctc ggc gca cgc gta aaa gtc gga gct cgc gac tcc Thr Phe Ser Ala Leu Gly Ala Arg Val Lys Val Gly Ala Arg Asp Ser 175 180 185			1061
gcc cac ctc gcc aga atc atg gag atg ggc ctc act cct ttc cac aca Ala His Leu Ala Arg Ile Met Glu Met Gly Leu Thr Pro Phe His Thr 190 195 200			1109
aac gaa ctt gca gag cat gtt gaa aat atc gac ata tgc atc aat acc Asn Glu Leu Ala Glu His Val Glu Asn Ile Asp Ile Cys Ile Asn Thr 205 210 215			1157
att cca agc ctg att ctc gat aaa cat gtc ctc tca cga atg aca ccc Ile Pro Ser Leu Ile Leu Asp Lys His Val Leu Ser Arg Met Thr Pro 220 225 230 235			1205
aga aca tta att ctc gat tta gca acc cgt ccc gga ggc aca gat ttt Arg Thr Leu Ile Leu Asp Leu Ala Thr Arg Pro Gly Gly Thr Asp Phe 240 245 250			1253
gat ttt gcc gaa aag caa ggc att aaa gcg ctg ctt gct cca gga ctt Asp Phe Ala Glu Lys Gln Gly Ile Lys Ala Leu Leu Ala Pro Gly Leu 255 260 265			1301
ccc ggg atc gtc gcg cct aaa acg gcg gga cag atc att gcc aat gtt Pro Gly Ile Val Ala Pro Lys Thr Ala Gly Gln Ile Ile Ala Asn Val 270 275 280			1349
ttg tgc aac ctt ttg tct gaa tta aca act gac cga aag ggg ctg tca Leu Cys Asn Leu Leu Ser Glu Leu Thr Thr Asp Arg Lys Gly Leu Ser 285 290 295			1397
taatgtcgat caaaggaaaa agaatcggat ttggcctaac gggttcacat tgtacgtatg			1457
atgccgtttt tccgcagatt gaagcgctga tcaacaaagg ggctgaagtc agaccggtcg			1517
tgacgcatac tgtcaagtcg acggatacac gctttggaga aggggaagaa tgggtcagaa			1577
gaatagaaga gctgactgga tttgaagtca ttgattccat tccgaaagct gagcctctcg			1637
ggccgaaaaac accgctggac tgcattggtt ttgcgccatt gacgggaaat tcgatgagca			1697
agcttgcaaa cgcccagacg gacagtccgg ttctcatggc ggccaaagcg acgatgagaa			1757
actcccgtcc cgtcgtcctc ggcatttcaa cgaatgacgc gtcgggcttg aacggcgtca			1817
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cttac			1882

10295.204.ST25.txt

<210> 93
 <211> 299
 <212> PRT
 <213> Bacillus licheniformis

<400> 93

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 Leu Glu Ile Ile Arg Lys Leu Thr Glu Gln Asp Ala Lys Val Phe Leu
 20 25 30
 Ile Gly Phe Asp Gln Leu Asp His Gly Phe Thr Gly Ala Thr Lys Leu
 35 40 45
 Lys Leu Asn Glu Leu Asp Phe Gly Thr Ile Asp Ser Ile Ile Leu Pro
 50 55 60
 Val Ser Gly Thr Ser Met Glu Gly Thr Val Ala Thr Val Phe Ser Asn
 65 70 75 80
 Glu Lys Val Val Leu Lys Gln Glu His Leu Glu Lys Thr Lys Pro His
 85 90 95
 Cys Ala Ile Tyr Ser Gly Ile Ser Asn Gln Tyr Leu Asp Gly Met Ala
 100 105 110
 Lys Gly Ala Asn Arg Arg Leu Ile Lys Leu Phe Glu Arg Asp Asp Ile
 115 120 125
 Ala Ile Tyr Asn Ser Ile Pro Thr Val Glu Gly Ala Ile Met Met Ala
 130 135 140
 Ile Gln His Thr Asp Phe Thr Ile His Gly Ser Asn Val Met Val Leu
 145 150 155 160
 Gly Leu Gly Arg Thr Gly Met Ser Ile Ser Arg Thr Phe Ser Ala Leu
 165 170 175
 Gly Ala Arg Val Lys Val Gly Ala Arg Asp Ser Ala His Leu Ala Arg
 180 185 190
 Ile Met Glu Met Gly Leu Thr Pro Phe His Thr Asn Glu Leu Ala Glu
 195 200 205
 His Val Glu Asn Ile Asp Ile Cys Ile Asn Thr Ile Pro Ser Leu Ile
 210 215 220
 Leu Asp Lys His Val Leu Ser Arg Met Thr Pro Arg Thr Leu Ile Leu
 225 230 235 240

10295.204.ST25.txt

Asp Leu Ala Thr Arg Pro Gly Gly Thr Asp Phe Asp Phe Ala Glu Lys
 245 250 255

Gln Gly Ile Lys Ala Leu Leu Ala Pro Gly Leu Pro Gly Ile Val Ala
 260 265 270

Pro Lys Thr Ala Gly Gln Ile Ile Ala Asn Val Leu Cys Asn Leu Leu
 275 280 285

Ser Glu Leu Thr Thr Asp Arg Lys Gly Leu Ser
 290 295

<210> 94
 <211> 1588
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1088)

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 ggctcgaatg taatggttct cgggctgggg cggacgggaa tgagcatcag ccggacgttc 120
 tcggcgctcg gcgcacgcgt aaaagtcgga gctcgcgact ccgcccacct cgccagaatc 180
 atggagatgg gcctcactcc tttccacaca aacgaacttg cagagcatgt tgaaaatatc 240
 gacatatgca tcaataccat tccaagcctg attctcgata aacatgtcct ctcacgaatg 300
 acaccagaa cattaattct cgatttagca acccgccccg gaggcacaga ttttgatttt 360
 gccgaaaagc aaggcattaa agcgtgctt gctccaggac ttcccgggat cgtcgcgcct 420
 aaaacggcgg gacagatcat tgccaatgtt ttgtgcaacc ttttgtctga attaacaact 480
 gaccgaaagg ggctgtcata atg tgc atc aaa gga aaa aga atc gga ttt ggc 533
 Met Ser Ile Lys Gly Lys Arg Ile Gly Phe Gly
 1 5 10
 cta acg ggt tca cat tgt acg tat gat gcc gtt ttt ccg cag att gaa 581
 Leu Thr Gly Ser His Cys Thr Tyr Asp Ala Val Phe Pro Gln Ile Glu
 15 20 25
 gcg ctg atc aac aaa ggg gct gaa gtc aga ccg gtc gtg acg cat act 629
 Ala Leu Ile Asn Lys Gly Ala Glu Val Arg Pro Val Val Thr His Thr
 30 35 40
 gtc aag tcg acg gat aca cgc ttt gga gaa ggg gaa gaa tgg gtc aga 677
 Val Lys Ser Thr Asp Thr Arg Phe Gly Glu Gly Glu Glu Trp Val Arg
 45 50 55
 aga ata gaa gag ctg act gga ttt gaa gtc att gat tcc att ccg aaa 725
 Arg Ile Glu Glu Leu Thr Gly Phe Glu Val Ile Asp Ser Ile Pro Lys
 60 65 70 75
 gct gag cct ctc ggg ccg aaa aca ccg ctg gac tgc atg gtt gtt gcg 773
 Ala Glu Pro Leu Gly Pro Lys Thr Pro Leu Asp Cys Met Val Val Ala
 80 85 90
 cca ttg acg gga aat tcg atg agc aag ctt gca aac gcc cag acg gac 821

10295.204.ST25.txt

Pro Leu Thr Gly Asn Ser Met Ser Lys Leu Ala Asn Ala Gln Thr Asp
 95 100 105

agt ccg gtt ctc atg gcg gcc aaa gcg acg atg aga aac tcc cgt ccc 869
 Ser Pro Val Leu Met Ala Ala Lys Ala Thr Met Arg Asn Ser Arg Pro
 110 115 120

gtc gtc ctc ggc att tca acg aat gac gcg ctc ggc ttg aac ggc gtc 917
 Val Val Leu Gly Ile Ser Thr Asn Asp Ala Leu Gly Leu Asn Gly Val
 125 130 135

aac ttg atg agg ctg atg gcg gca aaa aat gtt tac ttt att ccg ttc 965
 Asn Leu Met Arg Leu Met Ala Ala Lys Asn Val Tyr Phe Ile Pro Phe
 140 145 150 155

ggc cag gat gac cct tac aaa aag ccg aat tcg ctc gtc gcc aaa atg 1013
 Gly Gln Asp Asp Pro Tyr Lys Lys Pro Asn Ser Leu Val Ala Lys Met
 160 165 170

gat ctt tta gtg ccg gcg gtc gaa gaa gcg ctc tcc cat aaa caa ata 1061
 Asp Leu Leu Val Pro Ala Val Glu Glu Ala Leu Ser His Lys Gln Ile
 175 180 185

cag cct atc ctg gtc cat aat gat caa taaatctttt gaaaataaag 1108
 Gln Pro Ile Leu Val His Asn Asp Gln
 190 195

atgtaacaaa aaatatcaat caccacggca cacatctatg ttaaaataaa atgtaaaatg 1168

catagtcaac caatcgttta cgacgattaa ggtggaagga gttttacaat tgggcagagg 1228

attacatgta gcagtagttg gtgcgacagg cgctgtagga cagcaaagt taaaaacact 1288

agaagacagg aattttgaac tggataaaact gactttatta tcctcaaaac gttcagcagg 1348

tacgaaactg actttcaaag gcgaagagta cacagtagaa gaagctcgtc ctgagagctt 1408

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cgaggctgtc aaacgcgggg cgatcgtcat tgataatacg agcgcgttcc ggatggacca 1528

aaacactccg ctcgtcgtac ctgaggtcaa tgaggaagat ttgcacaagc acaacgggat 1588

<210> 95
 <211> 196
 <212> PRT
 <213> Bacillus licheniformis

<400> 95

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 1 5 10 15

Cys Thr Tyr Asp Ala Val Phe Pro Gln Ile Glu Ala Leu Ile Asn Lys
 20 25 30

Gly Ala Glu Val Arg Pro Val Val Thr His Thr Val Lys Ser Thr Asp
 35 40 45

Thr Arg Phe Gly Glu Gly Glu Glu Trp Val Arg Arg Ile Glu Glu Leu
 50 55 60

Thr Gly Phe Glu Val Ile Asp Ser Ile Pro Lys Ala Glu Pro Leu Gly
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10295.204.ST25.txt

65 70 - 75 80

Pro Lys Thr Pro Leu Asp Cys Met Val Val Ala Pro Leu Thr Gly Asn
85 90 95

Ser Met Ser Lys Leu Ala Asn Ala Gln Thr Asp Ser Pro Val Leu Met
100 105 110

Ala Ala Lys Ala Thr Met Arg Asn Ser Arg Pro Val Val Leu Gly Ile
115 120 125

Ser Thr Asn Asp Ala Leu Gly Leu Asn Gly Val Asn Leu Met Arg Leu
130 135 140

Met Ala Ala Lys Asn Val Tyr Phe Ile Pro Phe Gly Gln Asp Asp Pro
145 150 155 160

Tyr Lys Lys Pro Asn Ser Leu Val Ala Lys Met Asp Leu Leu Val Pro
165 170 175

Ala Val Glu Glu Ala Leu Ser His Lys Gln Ile Gln Pro Ile Leu Val
180 185 190

His Asn Asp Gln
195

<210> 96
<211> 2167
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1871)

<400> 96
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aggaatttct gaagctgcag agaaaaatgg cattccgtgt acattcaaca gggcgggggtc 120
tatgatcggc tttttcttca caaatggacc ggtcatcaat tatgatacag cgaaacagtc 180
tgacctcgga ctgtttgccg aatattataa aggaatggcc gatgaaggcg tgtttctgcc 240
gccttcacag tttgaagggc tgttcttgtc aaccgctcat acggatgacg acattgagca 300
tacgattaaa gctgctgaac gcgtattcga aagaatcagc cgctccagat aaagaaaagg 360
gctgccggac attgccggcg gctctttttt gcatggtgcc gaaaacggct gctgattttt 420
ctgttcatat tctgcctgct tttcacatac atctttactg acatctaatt ttaaaaatta 480
ggtgaaggga ggatatcagt ttg ccg caa aac aat cgt ttg caa ttt tct gta 533
Leu Pro Gln Asn Asn Arg Leu Gln Phe Ser Val
1 5 10
gaa gag tca atc tgt ttt caa aaa gga cag gaa gta tcc gaa tta tta 581
Glu Glu Ser Ile Cys Phe Gln Lys Gly Gln Glu Val Ser Glu Leu Leu

10295.204.ST25.txt

15

20

25

tcg att tca ttg gat cct gac att acc gtt cag gaa gta aat gat tat	629
Ser Ile Ser Leu Asp Pro Asp Ile Thr Val Gln Glu Val Asn Asp Tyr	
30 35 40	
gta tcc ata cga ggg tca tta gag ctg acc ggc gaa tac aac ata gat	677
Val Ser Ile Arg Gly Ser Leu Glu Leu Thr Gly Glu Tyr Asn Ile Asp	
45 50 55	
caa acc cgg gag tat gca gag ctg cct gcg acc agc cga ttt gta gaa	725
Gln Thr Arg Glu Tyr Ala Glu Leu Pro Ala Thr Ser Arg Phe Val Glu	
60 65 70 75	
gat gta aag ctg aaa ggg gac ggc agc gca gag ctg acg cat tgt ttc	773
Asp Val Lys Leu Lys Gly Asp Gly Ser Ala Glu Leu Thr His Cys Phe	
80 85 90	
cca gtg gat atc acc atc ccg aaa gac aaa gtc aat cat tta aac gac	821
Pro Val Asp Ile Thr Ile Pro Lys Asp Lys Val Asn His Leu Asn Asp	
95 100 105	
gta ttt gtt ttt att gac gct ttc gat tat cag ctg acc gat gcg agg	869
Val Phe Val Phe Ile Asp Ala Phe Asp Tyr Gln Leu Thr Asp Ala Arg	
110 115 120	
atg ctg acg att cag gct gat ttg gcg att gaa ggc ctc ttg aat gtg	917
Met Leu Thr Ile Gln Ala Asp Leu Ala Ile Glu Gly Leu Leu Asn Val	
125 130 135	
agc ggt gaa gcg ggt gaa gaa gaa ccg gcg act atg cct gcg gcc gtc	965
Ser Gly Glu Ala Gly Glu Glu Glu Pro Arg Thr Met Pro Ala Ala Val	
140 145 150 155	
cat ccg gaa gag gag ctc gaa cct gcc tac aga tca cct tca aac gac	1013
His Pro Glu Glu Glu Leu Glu Pro Ala Tyr Arg Ser Pro Ser Asn Asp	
160 165 170	
gaa gat cag ggt gaa gag aaa gaa tat ttg atc cag ctt gac aga cct	1061
Glu Asp Gln Gly Glu Glu Lys Glu Tyr Leu Ile Gln Leu Asp Arg Pro	
175 180 185	
tac gaa gag cag gac gaa gaa cag gcg gaa gaa cat gat acc ggt gag	1109
Tyr Glu Glu Gln Asp Glu Glu Gln Ala Glu Glu His Asp Thr Gly Glu	
190 195 200	
gaa acg gtt ccg att tac cag tcg ttt ctc gga aac gac acc gag gaa	1157
Glu Thr Val Pro Ile Tyr Gln Ser Phe Leu Gly Asn Asp Thr Glu Glu	
205 210 215	
gct aaa ccg ttt ttt acc gcg tct ttg tcg gcg gca gag cgt acg aag	1205
Ala Lys Pro Phe Phe Thr Ala Ser Leu Ser Ala Ala Glu Arg Thr Lys	
220 225 230 235	
cgc gaa ata gaa aat caa aaa gaa gcc tct ctt gaa cag ccg gaa gaa	1253
Arg Glu Ile Glu Asn Gln Lys Glu Ala Ser Leu Glu Gln Pro Glu Glu	
240 245 250	
gaa tat aag ctg aaa aga gag aaa gtg gaa gag gaa ccg gaa gaa tat	1301
Glu Tyr Lys Leu Lys Arg Glu Lys Val Glu Glu Glu Pro Glu Glu Tyr	
255 260 265	
gag ctg aaa aga gag aaa gtg gaa gag gaa ccg gaa gaa tat gag ctg	1349
Glu Leu Lys Arg Glu Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu	
270 275 280	
aaa aga gaa gaa gcg gaa gaa gag ccg gag ctg tcg cac agc tct tat	1397
Lys Arg Glu Glu Ala Glu Glu Glu Pro Glu Leu Ser His Ser Ser Tyr	

10295.204.ST25.txt

285 290 295

caa cct cac gag gaa ctg aaa gag aac ccg ttc tac agt gtt cct cct 1445
 Gln Pro His Glu Glu Leu Lys Glu Asn Pro Phe Tyr Ser Val Pro Pro
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ctt ctg aag gaa gac cag aat gac agg gag cct gag gct ttt gag gtt 1493
 Leu Leu Lys Glu Asp Gln Asn Asp Arg Glu Pro Glu Ala Phe Glu Val
 320 325 330

gag gtg aca cag gaa gca gaa gcg att gat gaa gaa gag gaa gcc ggg 1541
 Glu Val Thr Gln Glu Ala Glu Ala Ile Asp Glu Glu Glu Glu Ala Gly
 335 340 345

cat acg att gaa atc ccg gaa tat tcg ttt cat gag cag acg gag ccc 1589
 His Thr Ile Glu Ile Pro Glu Tyr Ser Phe His Glu Gln Thr Glu Pro
 350 355 360

gaa gaa gaa aga gat gaa atg cag gca gcg gat gaa cag gaa gtg tca 1637
 Glu Glu Glu Arg Asp Glu Met Gln Ala Ala Asp Glu Gln Glu Val Ser
 365 370 375

gca aag gaa aac gac aac gca ctc tat ttg aca aag ctg ttt aca aag 1685
 Ala Lys Glu Asn Asp Asn Ala Leu Tyr Leu Thr Lys Leu Phe Thr Lys
 380 385 390 395

cag gga gag gag gag ttt act cga atg agg atg tgc atc gtt cag caa 1733
 Gln Gly Glu Glu Glu Phe Thr Arg Met Arg Met Cys Ile Val Gln Gln
 400 405 410

aat gat acg att gat ctt ctg tgc gag cgc tat gat att aac gtc cag 1781
 Asn Asp Thr Ile Asp Leu Leu Cys Glu Arg Tyr Asp Ile Asn Val Gln
 415 420 425

cag ctc atc cgg atg aat tcc ctt tcc ctt gac gag gaa tta aaa gag 1829
 Gln Leu Ile Arg Met Asn Ser Leu Ser Leu Asp Glu Glu Leu Lys Glu
 430 435 440

gga cag atc ctt tat ata ccg gat tat caa aac agc cat gcc 1871
 Gly Gln Ile Leu Tyr Ile Pro Asp Tyr Gln Asn Ser His Ala
 445 450 455

taatgcattg ataaaaatgt ggtgaagccg atggaaggca tccagtctgt tttaaagag 1931

tacggtctta cgctgaata tatggagtcc gtcagttcaa aggtgtggaa agtgatatacg 1991

gatcacggtg tatttgctct gaaaaaattg gcggcttcaa gaaacacccg cttcacggaa 2051

cagatgatca tgctggagga aaaaggctac aggcagttcg ttcctgtcta tcgaaaccgc 2111

acaggcgaat ttttaacgca agccggagaa gatgtctgct atctcatgcc ctggct 2167

<210> 97

<211> 457

<212> PRT

<213> Bacillus licheniformis

<400> 97

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Phe Gln Lys Gly Gln Glu Val ser Glu Leu Leu ser Ile ser Leu Asp
 20 25 30

10295.204.ST25.txt

Pro Asp Ile Thr Val Gln Glu Val Asn Asp Tyr Val Ser Ile Arg Gly
 35 40 45

Ser Leu Glu Leu Thr Gly Glu Tyr Asn Ile Asp Gln Thr Arg Glu Tyr
 50 55 60

Ala Glu Leu Pro Ala Thr Ser Arg Phe Val Glu Asp Val Lys Leu Lys
 65 70 75 80

Gly Asp Gly Ser Ala Glu Leu Thr His Cys Phe Pro Val Asp Ile Thr
 85 90 95

Ile Pro Lys Asp Lys Val Asn His Leu Asn Asp Val Phe Val Phe Ile
 100 105 110

Asp Ala Phe Asp Tyr Gln Leu Thr Asp Ala Arg Met Leu Thr Ile Gln
 115 120 125

Ala Asp Leu Ala Ile Glu Gly Leu Leu Asn Val Ser Gly Glu Ala Gly
 130 135 140

Glu Glu Glu Pro Arg Thr Met Pro Ala Ala Val His Pro Glu Glu Glu
 145 150 155 160

Leu Glu Pro Ala Tyr Arg Ser Pro Ser Asn Asp Glu Asp Gln Gly Glu
 165 170 175

Glu Lys Glu Tyr Leu Ile Gln Leu Asp Arg Pro Tyr Glu Glu Gln Asp
 180 185 190

Glu Glu Gln Ala Glu Glu His Asp Thr Gly Glu Glu Thr Val Pro Ile
 195 200 205

Tyr Gln Ser Phe Leu Gly Asn Asp Thr Glu Glu Ala Lys Pro Phe Phe
 210 215 220

Thr Ala Ser Leu Ser Ala Ala Glu Arg Thr Lys Arg Glu Ile Glu Asn
 225 230 235 240

Gln Lys Glu Ala Ser Leu Glu Gln Pro Glu Glu Glu Tyr Lys Leu Lys
 245 250 255

Arg Glu Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu Lys Arg Glu
 260 265 270

Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu Lys Arg Glu Glu Ala
 275 280 285

Glu Glu Glu Pro Glu Leu Ser His Ser Ser Tyr Gln Pro His Glu Glu
 290 295 300

10295.204.ST25.txt

Leu Lys Glu Asn Pro Phe Tyr Ser Val Pro Pro Leu Leu Lys Glu Asp
 305 310 315 320

Gln Asn Asp Arg Glu Pro Glu Ala Phe Glu Val Glu Val Thr Gln Glu
 325 330 335

Ala Glu Ala Ile Asp Glu Glu Glu Glu Ala Gly His Thr Ile Glu Ile
 340 345 350

Pro Glu Tyr Ser Phe His Glu Gln Thr Glu Pro Glu Glu Glu Arg Asp
 355 360 365

Glu Met Gln Ala Ala Asp Glu Gln Glu Val Ser Ala Lys Glu Asn Asp
 370 375 380

Asn Ala Leu Tyr Leu Thr Lys Leu Phe Thr Lys Gln Gly Glu Glu Glu
 385 390 395 400

Phe Thr Arg Met Arg Met Cys Ile Val Gln Gln Asn Asp Thr Ile Asp
 405 410 415

Leu Leu Cys Glu Arg Tyr Asp Ile Asn Val Gln Gln Leu Ile Arg Met
 420 425 430

Asn Ser Leu Ser Leu Asp Glu Glu Leu Lys Glu Gly Gln Ile Leu Tyr
 435 440 445

Ile Pro Asp Tyr Gln Asn Ser His Ala
 450 455

<210> 98
 <211> 1955
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1463)

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 aaaaaggcga atttcatttc cttcaaatac aaaagacttt ggtgaagatc ccgctgtgaa 180
 acagggggaga gccgagcagc gcctgcagca catcttcaga cagattggct ccattccccg 240
 aaggacctca tcaatcacca ctttctcccg atttgccatg tcaacctgtt aagcatttac 300
 caaacaggat gaaaaaattg gtttgtccgc acagcttacc tgaatacaat aaaaaataaa 360
 gtatttctcg ggaaagcgca ggtttcaaca agacctgccc cgttcttgtc aaaaagcatt 420
 ggattgtgca gtcattgtgg cgctctgtcac ggcataagcg cgccatgaat aggatataaa 480
 gagagaatgg tgaggtgagt gtg ttg gaa agg gct gtt act tat aaa aac aac 533

10295.204.ST25.txt

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1 5 10

gga caa atc aat atc ata ttg aac ggt caa aag cag gtt ttg gcc aat 581
Gly Gln Ile Asn Ile Ile Leu Asn Gly Gln Lys Gln Val Leu Ala Asn
15 20 25

tca gag gct gaa gcc gaa tat cag gcc gca ctg caa aaa aat gaa gcc 629
Ser Glu Ala Glu Ala Glu Tyr Gln Ala Ala Leu Gln Lys Asn Glu Ala
30 35 40

aaa cac agc att ctg aaa gaa att gaa agg gaa atg aac acg ctg gtc 677
Lys His Ser Ile Leu Lys Glu Ile Glu Arg Glu Met Asn Thr Leu Val
45 50 55

gga atg gag gaa atg aag cgc aat atc aag gaa atc tac gcc tgg att 725
Gly Met Glu Glu Met Lys Arg Asn Ile Lys Glu Ile Tyr Ala Trp Ile
60 65 70 75

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Phe Val Asn Lys Lys Arg Glu Glu Gln Gly Leu Lys Ala Gly Lys Gln
80 85 90

gcg ctt cac atg atg ttc aaa gga aat ccg gga acc gga aaa acg acc 821
Ala Leu His Met Met Phe Lys Gly Asn Pro Gly Thr Gly Lys Thr Thr
95 100 105

gtc gcc agg ctg atc ggc agg ctt ttt tac gaa atg aat gtt ctc tca 869
Val Ala Arg Leu Ile Gly Arg Leu Phe Tyr Glu Met Asn Val Leu Ser
110 115 120

aaa ggc cat ctg atc gag ggc gag cgc gcc gat ctc gtc ggt gag tac 917
Lys Gly His Leu Ile Glu Ala Glu Arg Ala Asp Leu Val Gly Glu Tyr
125 130 135

atc ggc cat acg ggc caa aaa acg agg gat tta atc aaa aaa ggc atg 965
Ile Gly His Thr Ala Gln Lys Thr Arg Asp Leu Ile Lys Lys Ala Met
140 145 150 155

ggc gga atc ctg ttc atc gat gaa gcc tat tcc ctt gcc aga ggc gga 1013
Gly Gly Ile Leu Phe Ile Asp Glu Ala Tyr Ser Leu Ala Arg Gly Gly
160 165 170

gag aaa gac ttc ggc aag gag gca atc gat aca ttg gtc aaa cat atg 1061
Glu Lys Asp Phe Gly Lys Glu Ala Ile Asp Thr Leu Val Lys His Met
175 180 185

gag gat aag cgc aac gaa ttc att tta atc ctc gcc gga tat tcg cgg 1109
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190 195 200

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205 210 215

ccg atc agc atc gat ttt ccc gat tac tca gtc agc cag ctg atg gac 1205
Pro Ile Ser Ile Asp Phe Pro Asp Tyr Ser Val Ser Gln Leu Met Asp
220 225 230 235

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Ile Ala Lys Arg Met Met Ala Glu Arg Glu Tyr Gln Phe Ser Pro Glu
240 245 250

gct gaa tgg aag ctg aaa gac cat ctg atg gcc gtc aaa agt acg gtc 1301
Ala Glu Trp Lys Leu Lys Asp His Leu Met Ala Val Lys Ser Thr Val
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10295.204.ST25.txt

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 Lys Ser Ile Arg Ser Gln Ala Met Arg Leu Leu Met Gly Asp Cys Tyr
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 Glu Asp Ala Pro His Val
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Glu Tyr Gln Ala Ala Leu Gln Lys Asn Glu Ala Lys His Ser Ile Leu
 35 40 45

Lys Glu Ile Glu Arg Glu Met Asn Thr Leu Val Gly Met Glu Glu Met
 50 55 60

Lys Arg Asn Ile Lys Glu Ile Tyr Ala Trp Ile Phe Val Asn Lys Lys
 65 70 75 80

Arg Glu Glu Gln Gly Leu Lys Ala Gly Lys Gln Ala Leu His Met Met
 85 90 95

Phe Lys Gly Asn Pro Gly Thr Gly Lys Thr Thr Val Ala Arg Leu Ile
 100 105 110

Gly Arg Leu Phe Tyr Glu Met Asn Val Leu Ser Lys Gly His Leu Ile
 Page 140

10295.204.ST25.txt

115

120

125

Glu Ala Glu Arg Ala Asp Leu Val Gly Glu Tyr Ile Gly His Thr Ala
 130 135 140

Gln Lys Thr Arg Asp Leu Ile Lys Lys Ala Met Gly Gly Ile Leu Phe
 145 150 155 160

Ile Asp Glu Ala Tyr Ser Leu Ala Arg Gly Gly Glu Lys Asp Phe Gly
 165 170 175

Lys Glu Ala Ile Asp Thr Leu Val Lys His Met Glu Asp Lys Arg Asn
 180 185 190

Glu Phe Ile Leu Ile Leu Ala Gly Tyr Ser Arg Glu Met Asp His Phe
 195 200 205

Leu Ser Leu Asn Pro Gly Leu Gln Ser Arg Phe Pro Ile Ser Ile Asp
 210 215 220

Phe Pro Asp Tyr Ser Val Ser Gln Leu Met Asp Ile Ala Lys Arg Met
 225 230 235 240

Met Ala Glu Arg Glu Tyr Gln Phe Ser Pro Glu Ala Glu Trp Lys Leu
 245 250 255

Lys Asp His Leu Met Ala Val Lys Ser Thr Val Ser Pro Ala Lys Phe
 260 265 270

Ser Asn Gly Arg Phe Val Arg Asn Leu Ile Glu Lys Ser Ile Arg Ser
 275 280 285

Gln Ala Met Arg Leu Leu Met Gly Asp Cys Tyr Leu Lys Asn Asp Leu
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Val

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 <213> Bacillus licheniformis

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atntagagga ggaacaaagg atg atc ccg tta gtc aat tta aaa cgt caa ttt	533
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Gln Thr Val Lys Gln Asp Ile Leu Lys Glu Phe Glu His Val Leu Asp	
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Ser Gly Gln Tyr Ile Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg	
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Thr Asp Ala Leu Val Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly	
60 65 70 75	
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Asp Glu Val Ile Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala	
80 85 90	
gtc tca agg gtg ggg gct gaa cct gtg ttt gct gat gtc gat cct gaa	821
Val Ser Arg Val Gly Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu	
95 100 105	
aca tac aat ctt gat ccg aaa aaa ata gaa gaa aag atc acc cct gct	869
Thr Tyr Asn Leu Asp Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala	
110 115 120	
act aaa gcg atc att ccc gtc cat atc ttc gga cag ccg gct gat atg	917
Thr Lys Ala Ile Ile Pro Val His Ile Phe Gly Gln Pro Ala Asp Met	
125 130 135	
gac gag atc atg gag ctt gcc aaa aaa cac gga ctg ctt gtg att gag	965
Asp Glu Ile Met Glu Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu	
140 145 150 155	
gat gcc tgc caa gcg ttc ggc gca tcg tat aaa gag cgg cct gtc ggc	1013
Asp Ala Cys Gln Ala Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly	
160 165 170	
agc atc ggg gat gcc gcc tgt ttt tca ttt ttc cct aca aaa aac ttg	1061
Ser Ile Gly Asp Ala Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu	
175 180 185	
gga aca ttg gga gac ggg gga atg gtg acg att tca gac ccg gat gca	1109
Gly Thr Leu Gly Asp Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala	
190 195 200	
gcc cgg caa tta aga aca ctc aga acc cat ggc act agc aaa aaa tac	1157
Ala Arg Gln Leu Arg Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr	

10295.204.ST25.txt
215

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Ala Ala Leu Leu Ile Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln
 240 245 250

aga aga aga gtg gcc agc cgc tac aga gaa ggt ttg aaa acg gcg gag 1301
Arg Arg Arg Val Ala Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu
 255 260 265

cac ctc aca ctg ccg gca gag aaa gag gac cgc aca cat atc tat cat 1349
His Leu Thr Leu Pro Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His
 270 275 280

ctc tat tgt atc ggc gcg aaa aac cgc gac tac atc ata caa tcg ctg 1397
Leu Tyr Cys Ile Gly Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu
 285 290 295

aaa gag cag gac att cat tca ggt gtg tat tat cct tgc tgc ctt cat 1445
Lys Glu Gln Asp Ile His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His
300 305 310 315

ctg caa tcg gtc tat tct tca ctg cag tac aaa aaa ggc gat ttt cct 1493
Leu Gln Ser Val Tyr Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro
 320 325 330

ata gcc gag tcc ttg tcc gaa acc ctt ttc gcc att ccg atg gat cct 1541
Ile Ala Glu Ser Leu Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro
 335 340 345

ttt cta gcc gcc gag gaa caa gat cag att att tct gcg ctg ctg aaa 1589
Phe Leu Ala Ala Glu Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys
 350 355 360

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Lys Gly Gly Gly Glu Lys

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ccgtcagtga tttgcaggaa gaaagaatga aggaagcgga agaatactat gcttccctcg 1757

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<212> PRT
<213> Bacillus licheniformis

<400> 101

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10295.204.ST25.txt

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 50 55 60
 Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly Asp Glu Val Ile Thr
 65 70 75 80
 Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala Val Ser Arg Val Gly
 85 90 95
 Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu Thr Tyr Asn Leu Asp
 100 105 110
 Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala Thr Lys Ala Ile Ile
 115 120 125
 Pro Val His Ile Phe Gly Gln Pro Ala Asp Met Asp Glu Ile Met Glu
 130 135 140
 Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu Asp Ala Cys Gln Ala
 145 150 155 160
 Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly Ser Ile Gly Asp Ala
 165 170 175
 Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu Gly Thr Leu Gly Asp
 180 185 190
 Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala Ala Arg Gln Leu Arg
 195 200 205
 Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr Phe His Asp Lys Ile
 210 215 220
 Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala Ala Ala Leu Leu Ile
 225 230 235 240
 Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln Arg Arg Arg Val Ala
 245 250 255
 Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu His Leu Thr Leu Pro
 260 265 270
 Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His Leu Tyr Cys Ile Gly
 275 280 285

10295.204.ST25.txt

Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu Lys Glu Gln Asp Ile
 290 295 300

His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His Leu Gln Ser Val Tyr
 305 310 315 320

Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro Ile Ala Glu Ser Leu
 325 330 335

Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro Phe Leu Ala Ala Glu
 340 345 350

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Lys

<210> 102
 <211> 1975
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 actttcggaa tgaagttgaa caactttccc gtcgcgggat ttgtatgtaa aaaaaaacga 480
 aacaagcagg tgaacaattg atg agc gat atg aca gag tta tcc ggc cag cat 533
 Met Ser Asp Met Thr Glu Leu Ser Gly Gln His
 1 5 10
 att ttc ata act ggc gga gca ggc ttt atc gga tcc tct tta ata gga 581
 Ile Phe Ile Thr Gly Gly Ala Gly Phe Ile Gly Ser Ser Leu Ile Gly
 15 20 25
 aag ctg ata gag cgc aac agc gtc acc gta tat gac aat ttt tca aga 629
 Lys Leu Ile Glu Arg Asn Ser Val Thr Val Tyr Asp Asn Phe Ser Arg
 30 35 40
 gac tcc ctc cgg tat aag cct tac cgg gac cat cct cac ttg aaa gtg 677
 Asp Ser Leu Arg Tyr Lys Pro Tyr Arg Asp His Pro His Leu Lys Val
 45 50 55

10295.204.ST25.txt

ctg Leu 60	cag Gln 61	gga Gly 62	gac Asp 63	att Ile 64	ttg Leu 65	gat Asp 66	ttg Leu 67	aac Asn 68	gcg Ala 69	ctt Leu 70	aaa Lys 71	aag Lys 72	gcg Ala 73	atc Ile 74	cag Gln 75	725
ggg Gly 76	gcc Ala 77	agc Ser 78	cac His 79	att Ile 80	gtc Val 81	cac His 82	gcc Ala 83	gcc Ala 84	ggc Gly 85	atc Ile 86	gct Ala 87	ggg Gly 88	att Ile 89	gac Asp 90	acg Thr 91	773
gtc Val 92	att Ile 93	caa Gln 94	aac Asn 95	ccg Pro 96	gtt Val 97	aaa Lys 98	acg Thr 99	atg Met 100	cag Gln 101	gtc Val 102	aac Asn 103	atg Met 104	atc Ile 105	ggt Gly 106	tca Ser 107	821
gcc Ala 108	aat Asn 109	ctg Leu 110	ctt Leu 111	gaa Glu 112	gcg Ala 113	gct Ala 114	gcc Ala 115	ggt Gly 116	tta Leu 117	acc Thr 118	gaa Glu 119	tgc Cys 120	aaa Lys 121	agg Arg 122	gtt Val 123	869
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cgc Arg 140	gag Glu 141	acc Thr 142	agt Ser 143	cat His 144	act Thr 145	gtt Val 146	tta Leu 147	gga Gly 148	gcg Ala 149	gtg Val 150	gga Gly 151	gaa Glu 152	gcc Ala 153	cgc Arg 154	tgg Trp 155	965
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gaa Glu 252	cgc Arg 253	act Thr 254	gtg Val 255	atc Ile 256	acc Thr 257	gta Val 258	tac Tyr 259	gga Gly 260	ttg Leu 261	gca Ala 262	agc Ser 263	acg Thr 264	att Ile 265	atc Ile 266	aga Arg 267	1301
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gat Asp 284	att Ile 285	gaa Glu 286	ctg Leu 287	cgc Arg 288	atc Ile 289	cct Pro 290	cag Gln 291	gtc Val 292	aat Asn 293	aaa Lys 294	gca Ala 295	aaa Lys 296	gag Glu 297	atg Met 298	ctc Leu 299	1397
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gaa Glu 316	agc Ser 317	att Ile 318	aaa Lys 319	aaa Lys 320	aat Asn 321	ttg Leu 322	gat Asp 323	caa Gln 324	taagaaagga	ggcgctattg						1492

10295.204.ST25.txt

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 35 40 45

Lys Pro Tyr Arg Asp His Pro His Leu Lys Val Leu Gln Gly Asp Ile
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Leu Asp Leu Asn Ala Leu Lys Lys Ala Ile Gln Gly Ala Ser His Ile
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 85 90 95

Val Lys Thr Met Gln Val Asn Met Ile Gly Ser Ala Asn Leu Leu Glu
 100 105 110

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Ser Glu Val Phe Gly Gln Ile Ala Phe Arg Ala Arg Glu Thr Ser His
 130 135 140

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 145 150 155 160

Lys Leu Ala Glu Glu His Met Ala Tyr Ala Tyr Phe Lys Glu Leu Gly
 Page 147

10295.204.ST25.txt
170

165

175

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210 215 220

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225 230 235 240

Glu Ala Ile Gly Glu Ser Phe Asn Ile Gly Asn Glu Arg Thr Val Ile
245 250 255

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260 265 270

Ser Gln Ile Phe Phe Gly Glu Lys Lys Glu Ala Asp Ile Glu Leu Arg
275 280 285

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cgtacgatat cagcatacgt ccgtacgaag actgctgcac gatctttacg ctttctgcgc 240
cgaaaacgcg tccgaaaaaa gagaaaatcg aacactttga aagctacaca gatttcgaac 300
cgcttatcaa cgaagctgtg gaaaacacgg aaacgattgt tttgagcagc aaagcggaaa 360
cgaaagatca atttgcggat tttttctaaa ggaatattca atcaaacatc tttgtctggt 420

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<210> 106
<211> 1196
<212> DNA
<213> Bacillus licheniformis
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<220>
<221> CDS
<222> (501) .. (695)
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agggtatgcg cgggtccttg atcatgtgta ccagatcaaa gactatacgc tcaataaatc		180
ggcgcttgaa aaaatcgtca ttgagcagac tggacagctc cgcgattttt ataaagatct		240
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cgcttcgcac attcaggcga ccgcacattc catgattgac agcgtcttct taaaatatga		360
aatgaaataa tcgccgaccg gcgcgcctgg cttgccaatt gccaggcggt tttttgcctt		420
tcaacaattg ccagcataaa aagcctcagt ccaaatacaa ctaaacaagc agtaccaatt		480
gaaaaaggag ttgagaatgc atg gca aga acg aat aag ctc ctc gtt ccc ggg		533
Met Ala Arg Thr Asn Lys Leu Leu Val Pro Gly		
1 5 10		
gca gag cag gtt tta gac cag ttc aaa tac gaa atc gcc caa gag ttc		581
Ala Glu Gln Val Leu Asp Gln Phe Lys Tyr Glu Ile Ala Gln Glu Phe		
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Gly Val Gln Leu Gly Ser Asp Ser Val Ala Arg Ser Asn Gly Ser Val		
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Gly Gly Glu Met Thr Lys Arg Leu Val Gln Gln Ala Gln Ala Gln Leu		
45 50 55		
aat ggg cat aat gac aaa taaataccct atggattatt cgccggggccc		725
Asn Gly His Asn Asp Lys		
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gtcggcgga tattcttggt tattcgtttg gtcagaaggc tttttctcct tttggttaagg		785
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ttttttattt tcattgtcat catctttggt tttgtcttct aattcatctt tgtgggaacg		1145
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<210> 107
<211> 65
<212> PRT
<213> Bacillus licheniformis
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10295.204.ST25.txt

<400> 107

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Asp Gln Phe Lys Tyr Glu Ile Ala Gln Glu Phe Gly Val Gln Leu Gly
 20 25 30

Ser Asp Ser Val Ala Arg Ser Asn Gly Ser Val Gly Gly Glu Met Thr
 35 40 45

Lys Arg Leu Val Gln Gln Ala Gln Ala Gln Leu Asn Gly His Asn Asp
 50 55 60

Lys
 65

<210> 108
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 <212> DNA
 <213> Bacillus licheniformis

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 Val Lys Arg Gly Asp Thr Leu Tyr Gln Ile Ala 10
 1 5 10
 aat cgt tac cga aca aca gtt aat gaa att gtc gcg acg aat gaa att 581
 Asn Arg Tyr Arg Thr Thr Val Asn Glu Ile Val Ala Thr Asn Glu Ile 25
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 ccg aac ccg aat cgg ctt gtt gtc gga caa acc atc gtg atc ccg atc 629
 Pro Asn Pro Asn Arg Leu Val Val Gly Gln Thr Ile Val Ile Pro Ile 35 40
 30 35 40
 gcc gcc gag ttt tat gag gtc aga cag gga gat aca tta gca tca atc 677
 Ala Gly Glu Phe Tyr Glu Val Arg Gln Gly Asp Thr Leu Ala Ser Ile 55
 45 50 55
 gga gca cgc ttt aat att tct ccg gct gaa ctg gcg agg atc aac cgc 725
 Gly Ala Arg Phe Asn Ile Ser Pro Ala Glu Leu Ala Arg Ile Asn Arg
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10295.204.ST25.txt

60	65	70	75	
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cct cgg cca aga cgg aac att gaa aca aac gcc tat atc gaa cct cgg Pro Arg Pro Arg Asn Ile Glu Thr Asn Ala Tyr Ile Glu Pro Arg 95 100 105				821
gga gaa agc gta agc ccc gct ttg cag cag gcg gca aga gag gct tcg Gly Glu Ser Val Ser Pro Ala Leu Gln Gln Ala Ala Arg Glu Ala Ser 110 115 120				869
cca tac ttg acc tat ctg ggc gct ttc agc ttc cag gcg aag cgg gac Pro Tyr Leu Thr Tyr Leu Gly Ala Phe Ser Phe Gln Ala Lys Arg Asp 125 130 135				917
ggc aca ctc gaa gaa ccg ccg ctg aac aac tta aaa gaa att gcc gac Gly Thr Leu Glu Glu Pro Pro Leu Asn Asn Leu Lys Glu Ile Ala Asp 140 145 150 155				965
aga cat cgg act acg atg atg atg att gtc acc aat ctc gaa aat gaa Arg His Arg Thr Thr Met Met Ile Val Thr Asn Leu Glu Asn Glu 160 165 170				1013
gct ttc agc gac gaa ctc ggc agg atc att ctg acg gac cag aat gta Ala Phe Ser Asp Glu Leu Gly Arg Ile Ile Leu Thr Asp Gln Asn Val 175 180 185				1061
aaa aac aga ttg ctc gat aac atc gtt gca gcg gcc aga aga tac ggt Lys Asn Arg Leu Leu Asp Asn Ile Val Ala Ala Ala Arg Arg Tyr Gly 190 195 200				1109
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gaa ggc tgg ctc atc tca acc gcg ctt gct ccg aaa acg aga gcg gat Glu Gly Trp Leu Ile Ser Thr Ala Leu Ala Pro Lys Thr Arg Ala Asp 240 245 250				1253
cag ccc gga caa tgg tat gaa gcc cat gat tac ccg gcc cac ggc gaa Gln Pro Gly Gln Trp Tyr Glu Ala His Asp Tyr Arg Ala His Gly Glu 255 260 265				1301
att gtc gat ttc gtc gtg ctg atg aca tat gag tgg ggc tac agc gga Ile Val Asp Phe Val Val Leu Met Thr Tyr Glu Trp Gly Tyr Ser Gly 270 275 280				1349
ggg ccc ccg atg gcg gta tcg ccg atc ggg ccc gtc ccg gac gtg atc Gly Pro Pro Met Ala Val Ser Pro Ile Gly Pro Val Arg Asp Val Ile 285 290 295				1397
gaa tac gca ctc acg gaa atg ccc gcc agc aaa atc gtc atg gga cag Glu Tyr Ala Leu Thr Glu Met Pro Ala Ser Lys Ile Val Met Gly Gln 300 305 310 315				1445
aaa ctg tac ggc tat gac tgacgctccc ctatatgcac agcgggaccc Lys Leu Tyr Gly Tyr Asp 320				1493
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10295.204.ST25.txt

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ctttat 2279

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<210> 109
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 <212> PRT
 <213> Bacillus licheniformis

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 35 40 45

Glu Val Arg Gln Gly Asp Thr Leu Ala Ser Ile Gly Ala Arg Phe Asn
 50 55 60

Ile Ser Pro Ala Glu Leu Ala Arg Ile Asn Arg Ile Gln Val Ser Ala
 65 70 75 80

Val Leu Pro Val Gly Leu Leu Leu Tyr Ile Pro Pro Arg Pro Arg Arg
 85 90 95

Asn Ile Glu Thr Asn Ala Tyr Ile Glu Pro Arg Gly Glu Ser Val Ser
 100 105 110

Pro Ala Leu Gln Gln Ala Ala Arg Glu Ala Ser Pro Tyr Leu Thr Tyr
 115 120 125

Leu Gly Ala Phe Ser Phe Gln Ala Lys Arg Asp Gly Thr Leu Glu Glu
 130 135 140

10295.204.ST25.txt

Pro Pro Leu Asn Asn Leu Lys Glu Ile Ala Asp Arg His Arg Thr Thr
145 150 155 160

Met Met Met Ile Val Thr Asn Leu Glu Asn Glu Ala Phe Ser Asp Glu
165 170 175

Leu Gly Arg Ile Ile Leu Thr Asp Gln Asn Val Lys Asn Arg Leu Leu
180 185 190

Asp Asn Ile Val Ala Ala Ala Arg Arg Tyr Gly Phe Lys Asp Ile His
195 200 205

Phe Asp Phe Glu Tyr Leu Arg Pro Glu Asp Arg Glu Ala Tyr Asn Gln
210 215 220

Phe Leu Arg Asp Ala Arg Ala Arg Phe Arg Gln Glu Gly Trp Leu Ile
225 230 235 240

Ser Thr Ala Leu Ala Pro Lys Thr Arg Ala Asp Gln Pro Gly Gln Trp
245 250 255

Tyr Glu Ala His Asp Tyr Arg Ala His Gly Glu Ile Val Asp Phe Val
260 265 270

Val Leu Met Thr Tyr Glu Trp Gly Tyr Ser Gly Gly Pro Pro Met Ala
275 280 285

Val Ser Pro Ile Gly Pro Val Arg Asp Val Ile Glu Tyr Ala Leu Thr
290 295 300

Glu Met Pro Ala Ser Lys Ile Val Met Gly Gln Lys Leu Tyr Gly Tyr
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Asp

<210> 110
<211> 2011
<212> DNA
<213> Bacillus licheniformis

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aagaattatc cgcttcacgg ttctattcac cattccagct gtaaaaaacg gcgcatgac 180
cttctgcaac ggtcatagac atagcataaa accccctgtc acatacagag gaacaaaagg 240

10295.204.ST25.txt

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	Leu	Phe	Ile	Tyr	Thr	Val	Gln	Pro	Gly	Asp	Ser	Leu	Phe	
	1				5					10				
gtc atc ggc gcc aag ttc gga att tcg att gac cag atc cga ttg gcg	338													
Val Ile Gly Ala Lys Phe Gly Ile Ser Ile Asp Gln Ile Arg Leu Ala														
	15				20				25					
aat ggg ttg atc gca aca aac att gtc ccc gga cag gct ctt tta ata	386													
Asn Gly Leu Ile Ala Thr Asn Ile Val Pro Gly Gln Ala Leu Leu Ile														
	30				35				40				45	
ccg ctt tat aca tat acc gtt cag ccg gga gac agt tat tac acg att	434													
Pro Leu Tyr Thr Tyr Thr Val Gln Pro Gly Asp Ser Tyr Tyr Thr Ile														
				50				55				60		
gcc cgc cgg acg ttt gta tcc gtc gaa gca ttg caa aaa gca aat ccg	482													
Ala Arg Arg Thr Phe Val Ser Val Glu Ala Leu Gln Lys Ala Asn Pro														
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tct gta acc cct tcc aat atg agg ccg ggg ata aaa gtg atg att ccg	530													
Ser Val Thr Pro Ser Asn Met Arg Pro Gly Ile Lys Val Met Ile Pro														
				80				85				90		
gaa ttg ccg aaa aaa ccg atc act gct tta gga tat tac aca ctg aga	578													
Glu Leu Pro Lys Lys Pro Ile Thr Ala Leu Gly Tyr Tyr Thr Leu Arg														
				95				100				105		
aac ccc cgg tta gac cag gaa ttg att cat aat ttt gcc cca tac gcc	626													
Asn Pro Arg Leu Asp Gln Glu Leu Ile His Asn Phe Ala Pro Tyr Ala														
				110				115				120		125
acg tat ctg gca ttt ttt gaa tac cac att tca agc gac gga tcg tta	674													
Thr Tyr Leu Ala Phe Phe Glu Tyr His Ile Ser Ser Asp Gly Ser Leu														
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agc gag ctg aat gat tca ccg gcc gta caa acg gct tgg aga cgg cgc	722													
Ser Glu Leu Asn Asp Ser Pro Ala Val Gln Thr Ala Trp Arg Arg Arg														
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gtt cct ccc ctc atg aca gtc acc aat cta act gaa tca ggc ttc agt	770													
Val Pro Pro Leu Met Thr Val Thr Asn Leu Thr Glu Ser Gly Phe Ser														
				160				165				170		
ccg tct ctt gcg cac cgc gta tta aat cag cct gcc gta aga aat cgc	818													
Pro Ser Leu Ala His Arg Val Leu Asn Gln Pro Ala Val Arg Asn Arg														
				175				180				185		
ctc atc gac aat att gtc caa acg att tcc aga aaa gga tat gca ggc	866													
Leu Ile Asp Asn Ile Val Gln Thr Ile Ser Arg Lys Gly Tyr Ala Gly														
				190				195				200		205
gtc aat att gat ttc gaa cag att ttg gag gaa gac aga gat tta ttt	914													
Val Asn Ile Asp Phe Glu Gln Ile Leu Glu Glu Asp Arg Asp Leu Phe														
				210				215				220		
tca ggt ttt ctc cgc ctg ttg aaa gag ccg ctg aag ccg tcc ggc tat	962													
Ser Gly Phe Leu Arg Leu Leu Lys Glu Arg Leu Lys Pro Ser Gly Tyr														
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Val Leu Thr Ile Ala Val Pro Pro Lys Thr Asn Glu Asn Ile Ala Trp														
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ctg aaa ggg tat gac tat ggc gga atc ggt gca gtg agc gac ctt atc	1058													
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10295.204.ST25.txt

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270 275

att gct ccg atc aat gaa gtc cgg caa aca att caa ttt gct ctc cgc 1154
Ile Ala Pro Ile Asn Glu Val Arg Gln Thr Ile Gln Phe Ala Leu Arg 300
290 295 300

cat gtc ccc aaa gaa aaa atc gtt ctc ggc ttt ccg ctt tac ggc tat 1202
His Val Pro Lys Glu Lys Ile Val Leu Gly Phe Pro Leu Tyr Gly Tyr 315
305 310 315

aac tgg acc ctg ccc tat cag ccc ggt gcc gta tac ccc gga atc gcc 1250
Asn Trp Thr Leu Pro Tyr Gln Pro Gly Ala Val Tyr Pro Gly Ile Ala 330
320 325 330

aac caa gac gcc gtt cag ctc gcc atg aag cac cag gca ccg att caa 1298
Asn Gln Asp Ala Val Gln Leu Ala Met Lys His Gln Ala Pro Ile Gln 345
335 340 345

tat gat aca aat tct gag tcc cct ttt ttc aga tac acc gat gaa cag 1346
Tyr Asp Thr Asn Ser Glu Ser Pro Phe Phe Arg Tyr Thr Asp Glu Gln 365
350 355 360 365

ggc aga cgg cat gtc gta tgg ttt gaa gac gca cgc agc atc gga aaa 1394
Gly Arg Arg His Val Val Trp Phe Glu Asp Ala Arg Ser Ile Gly Lys 380
370 375 380

aaa ctg cag ctg atc acc gaa tac gga ctt gac ggc ggc ggc gtc tgg 1442
Lys Leu Gln Leu Ile Thr Glu Tyr Gly Leu Asp Gly Gly Gly Val Trp 395
385 390 395

cag ctc aca ctc agt ttt ccg caa gga aca tgg ctc ttg acc aaa ttc 1490
Gln Leu Thr 400 Leu Ser Phe Pro Gln Gly Thr Trp Leu Leu Thr Lys Phe 410
405 410

ttt cgc gtc cga aaa gtc tgacatcatt atgtgattta ttgtaaaata 1538
Phe Val Arg Lys Val 415

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caaatttgaa aggaatgttt gcgattgaat aatgcgatcc atgaaacatt ggagctgcat 1658
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<210> 111
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<213> Bacillus licheniformis

<400> 111

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10295.204.ST25.txt

Ala Lys Phe Gly Ile Ser Ile Asp Gln Ile Arg Leu Ala Asn Gly Leu
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Ile Ala Thr Asn Ile Val Pro Gly Gln Ala Leu Leu Ile Pro Leu Tyr
35 40 45

Thr Tyr Thr Val Gln Pro Gly Asp Ser Tyr Tyr Thr Ile Ala Arg Arg
50 55 60

Thr Phe Val Ser Val Glu Ala Leu Gln Lys Ala Asn Pro Ser Val Thr
65 70 75 80

Pro Ser Asn Met Arg Pro Gly Ile Lys Val Met Ile Pro Glu Leu Pro
85 90 95

Lys Lys Pro Ile Thr Ala Leu Gly Tyr Tyr Thr Leu Arg Asn Pro Arg
100 105 110

Leu Asp Gln Glu Leu Ile His Asn Phe Ala Pro Tyr Ala Thr Tyr Leu
115 120 125

Ala Phe Phe Glu Tyr His Ile Ser Ser Asp Gly Ser Leu Ser Glu Leu
130 135 140

Asn Asp Ser Pro Ala Val Gln Thr Ala Trp Arg Arg Arg Val Pro Pro
145 150 155 160

Leu Met Thr Val Thr Asn Leu Thr Glu Ser Gly Phe Ser Pro Ser Leu
165 170 175

Ala His Arg Val Leu Asn Gln Pro Ala Val Arg Asn Arg Leu Ile Asp
180 185 190

Asn Ile Val Gln Thr Ile Ser Arg Lys Gly Tyr Ala Gly Val Asn Ile
195 200 205

Asp Phe Glu Gln Ile Leu Glu Glu Asp Arg Asp Leu Phe Ser Gly Phe
210 215 220

Leu Arg Leu Leu Lys Glu Arg Leu Lys Pro Ser Gly Tyr Val Leu Thr
225 230 235 240

Ile Ala Val Pro Pro Lys Thr Asn Glu Asn Ile Ala Trp Leu Lys Gly
245 250 255

Tyr Asp Tyr Gly Gly Ile Gly Ala Val Ser Asp Leu Ile Phe Ile Met
260 265 270

Ala Tyr Asp Trp His His Gly Thr Ser Glu Pro Gly Pro Ile Ala Pro
275 280 285

10295.204.ST25.txt

Ile Asn Glu Val Arg Gln Thr Ile Gln Phe Ala Leu Arg His Val Pro
 290 295 300

Lys Glu Lys Ile Val Leu Gly Phe Pro Leu Tyr Gly Tyr Asn Trp Thr
 305 310 315 320

Leu Pro Tyr Gln Pro Gly Ala Val Tyr Pro Gly Ile Ala Asn Gln Asp
 325 330 335

Ala Val Gln Leu Ala Met Lys His Gln Ala Pro Ile Gln Tyr Asp Thr
 340 345 350

Asn Ser Glu Ser Pro Phe Phe Arg Tyr Thr Asp Glu Gln Gly Arg Arg
 355 360 365

His Val Val Trp Phe Glu Asp Ala Arg Ser Ile Gly Lys Lys Leu Gln
 370 375 380

Leu Ile Thr Glu Tyr Gly Leu Asp Gly Gly Gly Val Trp Gln Leu Thr
 385 390 395 400

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 405 410 415

Arg Lys Val

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 <212> DNA
 <213> Bacillus licheniformis

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 ttcgcgtggt cctgcctgcg aacatcatag caaaacttta gaaatccgaa caagtctgta 480
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 atagggggct ggtcacc atg aaa aaa aca tcg ggt tcg ctg cct tat ttt 590
 Met Lys Lys Thr Ser Gly Ser Leu Pro Tyr Phe

10295.204.ST25.txt

1

5

10

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Gln Asp Leu Ser Gln Glu Asn Leu Phe Leu Lys Ala Glu Leu Ala Arg	
15 20 25	
tca cat caa ttg ata cac gag ctt gaa gca agc tat ttt cac cag aaa	686
Ser His Gln Leu Ile His Glu Leu Glu Ala Ser Tyr Phe His Gln Lys	
30 35 40	
aat cat aag ctc agc cgg gaa aac gca gca atg aaa cag cag ctt cag	734
Asn His Lys Leu Ser Arg Glu Asn Ala Ala Met Lys Gln Gln Leu Gln	
45 50 55	
cag ctg tca ttc gaa ctg gag cgg att tcg gca aac aag gaa gac aag	782
Gln Leu Ser Phe Glu Leu Glu Arg Ile Ser Ala Asn Lys Glu Asp Lys	
60 65 70 75	
tcg gcc gaa acg ctc aac cgg ata aaa agc gaa ttg ctg agt aaa atc	830
Ser Ala Glu Thr Leu Asn Arg Ile Lys Ser Glu Leu Leu Ser Lys Ile	
80 85 90	
gtc gtt ctt cag gag ctt ctt caa aaa gaa acc tat gca aga aaa caa	878
Val Val Leu Gln Glu Leu Leu Gln Lys Glu Thr Tyr Ala Arg Lys Gln	
95 100 105	
gag ata gaa gaa aag cac cgc ctt cat tta aca aat gta aaa gcc gaa	926
Glu Ile Glu Glu Lys His Arg Leu His Leu Thr Asn Val Lys Ala Glu	
110 115 120	
gaa gag aaa aaa agc tta cat agc caa ata gaa tac gaa aag ctt cat	974
Glu Glu Lys Lys Ser Leu His Ser Gln Ile Glu Tyr Glu Lys Leu His	
125 130 135	
gca gaa aga gaa aaa acg ctg agg gaa aaa aag gaa cag gag ctc aaa	1022
Ala Glu Arg Glu Lys Thr Leu Arg Glu Lys Lys Glu Gln Glu Leu Lys	
140 145 150 155	
aac gct gca tac gaa aat gcc cgc ctg aaa gat gaa ctt cat gct aaa	1070
Asn Ala Ala Tyr Glu Asn Ala Arg Leu Lys Asp Glu Leu His Ala Lys	
160 165 170	
agt ctt cag ctc aaa caa atc gaa act gat gtt gcg gta tta aaa gag	1118
Ser Leu Gln Leu Lys Gln Ile Glu Thr Asp Val Ala Val Leu Lys Glu	
175 180 185	
cgg gtg acg gaa acg aaa agc cgg ctt ttg gag gct gaa aaa aca aaa	1166
Arg Val Thr Glu Thr Lys Ser Arg Leu Leu Glu Ala Glu Lys Thr Lys	
190 195 200	
gaa gcg ctg ttt tat gaa acg att ctc tct tat aaa agg caa ctc gat	1214
Glu Ala Leu Phe Tyr Glu Thr Ile Leu Ser Tyr Lys Arg Gln Leu Asp	
205 210 215	
gaa agt gat aag tgg atc gct tct cat ttt gcc gat att gat gca ttt	1262
Glu Ser Asp Lys Trp Ile Ala Ser His Phe Ala Asp Ile Asp Ala Phe	
220 225 230 235	
cag cag acg gag aag gcg ctt gaa caa aac gag gag gtt ttt gaa cgg	1310
Gln Gln Thr Glu Lys Ala Leu Glu Gln Asn Glu Glu Val Phe Glu Arg	
240 245 250	
aca gaa cag atc gag gcg gtg ctt caa act gtt aca gag caa gtt gat	1358
Thr Glu Gln Ile Glu Ala Val Leu Gln Thr Val Thr Glu Gln Val Asp	
255 260 265	
cag ctc caa caa caa ttg agc gcc att caa caa aat tat acg aaa atg	1406
Gln Leu Gln Gln Gln Leu Ser Ala Ile Gln Gln Asn Tyr Thr Lys Met	

10295.204.ST25.txt

270

275

280

gat caa aaa ata aca gaa tgg aaa aaa cag gcg aaa gaa gaa aca ccc 1454
 Asp Gln Lys Ile Thr Glu Trp Lys Lys Gln Ala Lys Glu Glu Thr Pro
 285 290 295

ccg caa aaa tgg gtc tat caa att aaa cgc aaa gac aaa gaa aca aaa 1502
 Pro Gln Lys Trp Val Tyr Gln Ile Lys Arg Lys Asp Lys Glu Thr Lys
 300 305 310 315

cct tta aat taaataccac ttaaggaat aatttggttt ttacaaaaaa 1551
 Pro Leu Asn

accgcttgag tagattgtct caagcagttg attgggcggc ggcgtataaa gcggccgcct 1611

ttatgttccc ttaaaatgga aacgctatct gaaaaagcaa gggtttgacc tattgctgct 1671

ctgtctcagt agaaatctca ccctctaata tatattgacc gcggtatggt tttttgactt 1731

ccgggtacat ttaaatcagg ctttgcataa aggttgtcat attagggatc tcaagtccgc 1791

tctctttttc gatttctttt tgaagttcgg agcttttgat ggccgcatta tggcgtttta 1851

atgttttaaat cgccgcttca cgcaattttg cagcttttga gcctggacgt gctgtacccc 1911

ttctgcgcct tgcgtttcca tctggaattc cggcaggcag tgaggagggt tgcggagaag 1971

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<210> 113

<211> 318

<212> PRT

<213> Bacillus licheniformis

<400> 113

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Glu Asn Leu Phe Leu Lys Ala Glu Leu Ala Arg Ser His Gln Leu Ile
 20 25 30

His Glu Leu Glu Ala Ser Tyr Phe His Gln Lys Asn His Lys Leu Ser
 35 40 45

Arg Glu Asn Ala Ala Met Lys Gln Gln Leu Gln Gln Leu Ser Phe Glu
 50 55 60

Leu Glu Arg Ile Ser Ala Asn Lys Glu Asp Lys Ser Ala Glu Thr Leu
 65 70 75 80

Asn Arg Ile Lys Ser Glu Leu Leu Ser Lys Ile Val Val Leu Gln Glu
 85 90 95

Leu Leu Gln Lys Glu Thr Tyr Ala Arg Lys Gln Glu Ile Glu Glu Lys
 100 105 110

His Arg Leu His Leu Thr Asn Val Lys Ala Glu Glu Glu Lys Lys Ser
 115 120 125

10295.204.ST25.txt

Leu His Ser Gln Ile Glu Tyr Glu Lys Leu His Ala Glu Arg Glu Lys
 130 135 140

Thr Leu Arg Glu Lys Lys Glu Gln Glu Leu Lys Asn Ala Ala Tyr Glu
 145 150 155 160

Asn Ala Arg Leu Lys Asp Glu Leu His Ala Lys Ser Leu Gln Leu Lys
 165 170 175

Gln Ile Glu Thr Asp Val Ala Val Leu Lys Glu Arg Val Thr Glu Thr
 180 185 190

Lys Ser Arg Leu Leu Glu Ala Glu Lys Thr Lys Glu Ala Leu Phe Tyr
 195 200 205

Glu Thr Ile Leu Ser Tyr Lys Arg Gln Leu Asp Glu Ser Asp Lys Trp
 210 215 220

Ile Ala Ser His Phe Ala Asp Ile Asp Ala Phe Gln Gln Thr Glu Lys
 225 230 235 240

Ala Leu Glu Gln Asn Glu Glu Val Phe Glu Arg Thr Glu Gln Ile Glu
 245 250 255

Ala Val Leu Gln Thr Val Thr Glu Gln Val Asp Gln Leu Gln Gln Gln
 260 265 270

Leu Ser Ala Ile Gln Gln Asn Tyr Thr Lys Met Asp Gln Lys Ile Thr
 275 280 285

Glu Trp Lys Lys Gln Ala Lys Glu Glu Thr Pro Pro Gln Lys Trp Val
 290 295 300

Tyr Gln Ile Lys Arg Lys Asp Lys Glu Thr Lys Pro Leu Asn
 305 310 315

<210> 114
 <211> 2341
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1838)

<400> 114
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 agcccgttct aaacggcagc atcgagaaaa aagcagaccg cgaatcagtg gaagctgtgg 180
 aagaagcggg agatcaaaaat aaaaaagaaa cagaagcttt atttttctat aatccccgaca 240

10295.204.ST25.txt

tcgcttctga tgactggatt aaaacgagaa aagtcgtgaa gcgcatacggc aatcatgtct	300
ttgcgatcta gaaagcagtc agggccattc gccttggtcg ctttttttgt gcgattcttt	360
cttacgcatt atcatctttc acagcccaag aaaaaattta tttttgatac tttatgaaaa	420
tcaattttca attaaaaaga aaataatttt tagacttgtc tcatatgatg ggataaaccc	480
gtgagacaag gagagacctc atg aac cgt ttt gta aaa gga atc gtt ctt ctt	533
Met Asn Arg Phe Val Lys Gly Ile Val Leu Leu	
1 5 10	
tcg cta gct gct ttt ttt gca gaa tgt ctt gaa ttc gtc atc aac atg	581
Ser Leu Ala Ala Phe Phe Ala Glu Cys Leu Glu Phe Val Ile Asn Met	
15 20 25	
att ctt gca cgg gag ctt ggc gag cat ggc atg ggg ctc tac atg agt	629
Ile Leu Ala Arg Glu Leu Gly Glu His Gly Met Gly Leu Tyr Met Ser	
30 35 40	
gtt ttg cct tcc att ttt ttg gtc gtg gtg att gcg agc ctt gag ctg	677
Val Leu Pro Ser Ile Phe Leu Val Val Val Ile Ala Ser Leu Glu Leu	
45 50 55	
ccc gta tca ata tcg aag ttt atc gcc gag tcc aac ccg aag ctg cac	725
Pro Val Ser Ile Ser Lys Phe Ile Ala Glu Ser Asn Pro Lys Leu His	
60 65 70 75	
gaa agc atg ctg aaa cat gca ttg cgg atg act gcg gtc tgc acg gtt	773
Glu Ser Met Leu Lys His Ala Leu Arg Met Thr Ala Val Cys Thr Val	
80 85 90	
ttc tcc acg gca gcc gca gtg atc att ctt cca ttt att ccg gtt ttt	821
Phe Ser Thr Ala Ala Ala Val Ile Ile Leu Pro Phe Ile Pro Val Phe	
95 100 105	
gat tct tac cac cct cta atc aga gga ctt gtg atc ggg atg att cct	869
Asp Ser Tyr His Pro Leu Ile Arg Gly Leu Val Ile Gly Met Ile Pro	
110 115 120	
acg gtt gca ttc aca tcg atc gcg aga ggc tac ttc atg ggc gtt cag	917
Thr Val Ala Phe Thr Ser Ile Ala Arg Gly Tyr Phe Met Gly Val Gln	
125 130 135	
caa atg ggt aaa atc gca acg gcg aat gcc ttg aaa aaa atc ttt cag	965
Gln Met Gly Lys Ile Ala Thr Ala Asn Ala Leu Lys Lys Ile Phe Gln	
140 145 150 155	
ctc atc ggc ttg ttt tta ttt ttt caa tgg tat tcc ttt gaa ttg gat	1013
Leu Ile Gly Leu Phe Leu Phe Phe Gln Trp Tyr Ser Phe Glu Leu Asp	
160 165 170	
act tct ctt ctc att tca ttg ttt gtc ctc gtt gca agt gaa gtg gtc	1061
Thr Ser Leu Leu Ile Ser Leu Phe Val Leu Val Ala Ser Glu Val Val	
175 180 185	
gtg ttt gtt tat ttg ttt tcg cag ttt gtt ttg gtc agg cgt gcc gct	1109
Val Phe Val Tyr Leu Phe Ser Gln Phe Val Leu Val Arg Arg Ala Ala	
190 195 200	
caa aaa ggg cag cag atc cac ttg cgg aga aac gat gtt tta aaa cgc	1157
Gln Lys Gly Gln Gln Ile His Leu Arg Arg Asn Asp Val Leu Lys Arg	
205 210 215	
ctg ctc act gtt tcg atc ccg acg acg ggg ctg cgc gtg ttt cat gct	1205
Leu Leu Thr Val Ser Ile Pro Thr Thr Gly Leu Arg Val Phe His Ala	
220 225 230 235	

10295.204.ST25.txt

gtg aca aat gcc gtc gaa cct ttt ttg gtg aag ggg acg ctg ctt gcc 1253
 Val Thr Asn Ala Val Glu Pro Phe Leu Val Lys Gly Thr Leu Leu Ala
 240 245 250

gct ggc gta tca aga aca tcg gcc atc gac cag ttc ggc atg ctt tcg 1301
 Ala Gly Val Ser Arg Thr Ser Ala Ile Asp Gln Phe Gly Met Leu Ser
 255 260 265

gga gtt gcg atg aca atc ggc ttt ttt ccg gct ttt atc gcc cat tca 1349
 Gly Val Ala Met Thr Ile Gly Phe Phe Pro Ala Phe Ile Ala His Ser
 270 275 280

ctg atg gtc gtc atg atc ccg agc att tct gaa agc tac gct tac ggg 1397
 Leu Met Val Val Met Ile Pro Ser Ile Ser Glu Ser Tyr Ala Tyr Gly
 285 290 295

caa tac gaa aga gtg atc aaa cgg att aaa cag gcg atc ttt att acg 1445
 Gln Tyr Glu Arg Val Ile Lys Arg Ile Lys Gln Ala Ile Phe Ile Thr
 300 305 310 315

ctg ttt tac ggc ata ccg tcc gtc atg gtg atg tat cac ttt gca gag 1493
 Leu Phe Tyr Gly Ile Pro Ser Val Met Val Met Tyr His Phe Ala Glu
 320 325 330

ccg ctg acc cat tta ttt ttc gat tcg gtc aag gcg tcg ttt tac ctt 1541
 Pro Leu Thr His Leu Phe Phe Asp Ser Val Lys Ala Ser Phe Tyr Leu
 335 340 345

aaa atg ttg tgg ccg tat ttt tta ttc cac ttt ttt gcg atg cct ttt 1589
 Lys Met Leu Trp Pro Tyr Phe Leu Phe His Phe Phe Ala Met Pro Phe
 350 355 360

cag gcc tgt tta atc gga atg ggg ttg gcc aaa gat gct ttt tat cat 1637
 Gln Ala Cys Leu Ile Gly Met Gly Leu Ala Lys Asp Ala Phe Tyr His
 365 370 375

aac gtt tgg gcc agt gtc tta tcg ttt ttg atg atg tat gtt ctc ggg 1685
 Asn Val Trp Ala Ser Val Leu Ser Phe Leu Met Met Tyr Val Leu Gly
 380 385 390 395

tcc atg cag act ttg cag atg acg ggg atc att ctt gcg atg aat acc 1733
 Ser Met Gln Thr Leu Gln Met Thr Gly Ile Ile Leu Ala Met Asn Thr
 400 405 410

ggt atg att ttg ctg acg gcg ctg cat tat gtg acg att tgc aag gag 1781
 Gly Met Ile Leu Leu Thr Ala Leu His Tyr Val Thr Ile Cys Lys Glu
 415 420 425

ctg gcc gtc acg ctt ttt ttg aca aac aaa tcc cga tct ccg aga att 1829
 Leu Gly Val Thr Leu Phe Leu Thr Asn Lys Ser Arg Ser Pro Arg Ile
 430 435 440

gaa agc cgc tgatggatcc tcttcatagt tttagctttt gcggggaagc 1878
 Glu Ser Arg
 445

taatattaaa aaagaagggg agttcccatg cgaagaatca gtctcattta cccgctcatc 1938

ctgctgtttt ttaccggggtt attcgtattt cagccgcagg catctgcaaa acaagcttcg 1998

ccggcagtca tgcagatgaa cacggtcgaa ggtcagcgcg tcgtcattcc cgccgaaggc 2058

cagaagacga tcgttcattt ttggacgacc tgggtgccgc catgccgtga agagcttccg 2118

cgattccaat cctactatga aagcaagcaa tccggcgatca agctcgtgac cgtaatttta 2178

ctgaatgccg aaaagaacga acagaaggta aaacagttta ttaaagcaaa caagctgaca 2238

10295.204.ST25.txt

tttccgatcg tttttgacaa aaagggtgag atgatgaaag catataaagt catgacaatt 2298
 cctacgactt ttttcttttaa tgaaaaagga gagctggaga aaa 2341

<210> 115
 <211> 446
 <212> PRT
 <213> Bacillus licheniformis

<400> 115

Met Asn Arg Phe Val Lys Gly Ile Val Leu Leu Ser Leu Ala Ala Phe
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Phe Ala Glu Cys Leu Glu Phe Val Ile Asn Met Ile Leu Ala Arg Glu
 20 25 30

Leu Gly Glu His Gly Met Gly Leu Tyr Met Ser Val Leu Pro Ser Ile
 35 40 45

Phe Leu Val Val Val Ile Ala Ser Leu Glu Leu Pro Val Ser Ile Ser
 50 55 60

Lys Phe Ile Ala Glu Ser Asn Pro Lys Leu His Glu Ser Met Leu Lys
 65 70 75 80

His Ala Leu Arg Met Thr Ala Val Cys Thr Val Phe Ser Thr Ala Ala
 85 90 95

Ala Val Ile Ile Leu Pro Phe Ile Pro Val Phe Asp Ser Tyr His Pro
 100 105 110

Leu Ile Arg Gly Leu Val Ile Gly Met Ile Pro Thr Val Ala Phe Thr
 115 120 125

Ser Ile Ala Arg Gly Tyr Phe Met Gly Val Gln Gln Met Gly Lys Ile
 130 135 140

Ala Thr Ala Asn Ala Leu Lys Lys Ile Phe Gln Leu Ile Gly Leu Phe
 145 150 155 160

Leu Phe Phe Gln Trp Tyr Ser Phe Glu Leu Asp Thr Ser Leu Leu Ile
 165 170 175

Ser Leu Phe Val Leu Val Ala Ser Glu Val Val Val Phe Val Tyr Leu
 180 185 190

Phe Ser Gln Phe Val Leu Val Arg Arg Ala Ala Gln Lys Gly Gln Gln
 195 200 205

Ile His Leu Arg Arg Asn Asp Val Leu Lys Arg Leu Leu Thr Val Ser
 210 215 220

10295.204.ST25.txt

Ile Pro Thr Thr Gly Leu Arg Val Phe His Ala Val Thr Asn Ala Val
 225 230 235 240

Glu Pro Phe Leu Val Lys Gly Thr Leu Leu Ala Ala Gly Val Ser Arg
 245 250 255

Thr Ser Ala Ile Asp Gln Phe Gly Met Leu Ser Gly Val Ala Met Thr
 260 265 270

Ile Gly Phe Phe Pro Ala Phe Ile Ala His Ser Leu Met Val Val Met
 275 280 285

Ile Pro Ser Ile Ser Glu Ser Tyr Ala Tyr Gly Gln Tyr Glu Arg Val
 290 295 300

Ile Lys Arg Ile Lys Gln Ala Ile Phe Ile Thr Leu Phe Tyr Gly Ile
 305 310 315 320

Pro Ser Val Met Val Met Tyr His Phe Ala Glu Pro Leu Thr His Leu
 325 330 335

Phe Phe Asp Ser Val Lys Ala Ser Phe Tyr Leu Lys Met Leu Trp Pro
 340 345 350

Tyr Phe Leu Phe His Phe Phe Ala Met Pro Phe Gln Ala Cys Leu Ile
 355 360 365

Gly Met Gly Leu Ala Lys Asp Ala Phe Tyr His Asn Val Trp Ala Ser
 370 375 380

Val Leu Ser Phe Leu Met Met Tyr Val Leu Gly Ser Met Gln Thr Leu
 385 390 395 400

Gln Met Thr Gly Ile Ile Leu Ala Met Asn Thr Gly Met Ile Leu Leu
 405 410 415

Thr Ala Leu His Tyr Val Thr Ile Cys Lys Glu Leu Gly Val Thr Leu
 420 425 430

Phe Leu Thr Asn Lys Ser Arg Ser Pro Arg Ile Glu Ser Arg
 435 440 445

<210> 116
 <211> 1417
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (420)..(914)

<400> 116

10295.204.ST25.txt

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tgaggtgaca atcggaatgc ccgcctgggt gatcgccctca atatcccgat aaatcgttct	120
gacagagact tcgaacatgc cggcaagctc ctttgccctgc acttggcgtt tattaatcaa	180
taaaatcaca atggccaaaa gccgggtcaat tttcactgca gatccctcac attcatcttg	240
tgcagcctct ttttttctgc tattttcatt ccatagcgca caccattctg ggatatcatg	300
acaaaaaaga ggatctcatc acccatttat ctagaaaacc acttttcagg ttacgatttg	360
tacagtttgg acatatactc cttaaaaaag gaggttttaa aaacatcata ttttatttt	419
ttg cag ttt ttc atc att gtg tcc atc gtc tat atc aag ttc aaa cgg Leu Gln Phe Phe Ile Ile Val Ser Ile Val Tyr Ile Lys Phe Lys Arg 1 5 10 15	467
tcg gtc ggt tat cag cct tta aag ccg gca cgc atg ttg ttc cgg atc Ser Val Gly Tyr Gln Pro Leu Lys Pro Ala Arg Met Leu Phe Arg Ile 20 25 30	515
atc ctt ttt tcg gga att ttc gtt ttt ctg ctg acg atg agc gca ctt Ile Leu Phe Ser Gly Ile Phe Val Phe Leu Leu Thr Met Ser Ala Leu 35 40 45	563
cac cct tta tca tac ttt tat gat ctg att ggg atc gcg ctc gga ctc His Pro Leu Ser Tyr Phe Tyr Asp Leu Ile Gly Ile Ala Leu Gly Leu 50 55 60	611
atc ttg acc gtc tat gcg ctg aag cat gtg tcg atc gaa aat cgg ggc Ile Leu Thr Val Tyr Ala Leu Lys His Val Ser Ile Glu Asn Arg Gly 65 70 75 80	659
gga gtc ctt tat ttc aga acg cat tta tgg gtt gaa ttg atc gta ctc Gly Val Leu Tyr Phe Arg Thr His Leu Trp Val Glu Leu Ile Val Leu 85 90 95	707
ttt tta ttt tta tac cgg ttt ctg tac cgg atc gcc gag atc ggc cag Phe Leu Phe Leu Tyr Arg Phe Leu Tyr Arg Ile Ala Glu Ile Gly Gln 100 105 110	755
ctg cag act gcg gtt tca gac ggg ggt tcg gca gct tac ggc gcc ctt Leu Gln Thr Ala Val Ser Asp Gly Gly Ser Ala Ala Tyr Gly Ala Leu 115 120 125	803
ttt gcg cag gac ccg gcg acg atg atc ggt ttt ttt gta ctg gcc gtt Phe Ala Gln Asp Pro Ala Thr Met Ile Gly Phe Phe Val Leu Ala Val 130 135 140	851
tat tat gtc ggt ttc tct ttt ttt gtt tta aaa aaa ggc aga acc gaa Tyr Tyr Val Gly Phe Ser Phe Phe Val Leu Lys Lys Gly Arg Thr Glu 145 150 155 160	899
gaa aag cgc tca gct taaaaaggca aactcgggaa attgagtttg ccttttaaac Glu Lys Arg Ser Ala 165	954
tttagtcatg ttgtgtatga tcgatcatct gctgaagtac atcgaggaca tgctggctct	1014
ccggagaata aaaaatggaa gtccctgccc ttcttgattt gacgagacga aggtttttta	1074
aaaacctgag ctggtgagaa acgggtgact gcaggagact cagcttctct gctatttcat	1134
taaccgaatg ctcgccttgt gagagcaggt gaagaatttt gattctcggt gggtcagaga	1194
gcgctttaaa cgtctgtgaa acgagaaata aagtttcttc atctaactcg gcccgcacct	1254

10295.204.ST25.txt

gtttttctgt tggtttcttga ttgtgctcac tcatgctttt caccttttcc gcgcgacttt 1314
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 acagcgttcc ttgaagcgct tctacatatc ttgcagcaga cct 1417

<210> 117
 <211> 165
 <212> PRT
 <213> Bacillus licheniformis

<400> 117

Leu Gln Phe Phe Ile Ile Val Ser Ile Val Tyr Ile Lys Phe Lys Arg
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Ser Val Gly Tyr Gln Pro Leu Lys Pro Ala Arg Met Leu Phe Arg Ile
 20 25 30

Ile Leu Phe Ser Gly Ile Phe Val Phe Leu Leu Thr Met Ser Ala Leu
 35 40 45

His Pro Leu Ser Tyr Phe Tyr Asp Leu Ile Gly Ile Ala Leu Gly Leu
 50 55 60

Ile Leu Thr Val Tyr Ala Leu Lys His Val Ser Ile Glu Asn Arg Gly
 65 70 75 80

Gly Val Leu Tyr Phe Arg Thr His Leu Trp Val Glu Leu Ile Val Leu
 85 90 95

Phe Leu Phe Leu Tyr Arg Phe Leu Tyr Arg Ile Ala Glu Ile Gly Gln
 100 105 110

Leu Gln Thr Ala Val Ser Asp Gly Gly Ser Ala Ala Tyr Gly Ala Leu
 115 120 125

Phe Ala Gln Asp Pro Ala Thr Met Ile Gly Phe Phe Val Leu Ala Val
 130 135 140

Tyr Tyr Val Gly Phe Ser Phe Phe Val Leu Lys Lys Gly Arg Thr Glu
 145 150 155 160

Glu Lys Arg Ser Ala
 165

<210> 118
 <211> 2353
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1850)

[illegible]

10295.204.ST25.txt

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ata acc gaa aaa gaa gcg cgc aag att gcc caa aaa ttc gcc cag gac Ile Thr Glu Lys Glu Ala Arg Lys Ile Ala Gln Lys Phe Ala Gln Asp 220 225 230 235	1205
aaa aat tac aat atc aaa gta tcg aaa agc ggc aag aaa acg aac agg Lys Asn Tyr Asn Ile Lys Val Ser Lys Ser Gly Lys Lys Thr Asn Arg 240 245 250	1253
gat gta tac agc atc agt atg cag gac cct gat caa aaa gcg gat att Asp Val Tyr Ser Ile Ser Met Gln Asp Pro Asp Gln Lys Ala Asp Ile 255 260 265	1301
tat atg gac att acc gaa aaa ggc gga tat ccg gtt tat ctg att caa Tyr Met Asp Ile Thr Glu Lys Gly Gly Tyr Pro Val Tyr Leu Ile Gln 270 275 280	1349
aac aaa aaa att aaa gat gaa aaa atc agc tta aac gat gcg tca aac Asn Lys Lys Ile Lys Asp Glu Lys Ile Ser Leu Asn Asp Ala Ser Asn 285 290 295	1397
aaa gcc ctt caa ttt ttg aaa aaa aac ggc tat aaa acg gaa gac ctg Lys Ala Leu Gln Phe Leu Lys Lys Asn Gly Tyr Lys Thr Glu Asp Leu 300 305 310 315	1445
aag atg gat gaa agc tcg caa tac gac ggc gtc ggg gtg ttt tca ttt Lys Met Asp Glu Ser Ser Gln Tyr Asp Gly Val Gly Val Phe Ser Phe 320 325 330	1493
gtt ccg gtc cag gac gat gtc tgg ctc tat ccg gac agc atc cgc atc Val Pro Val Gln Asp Asp Val Trp Leu Tyr Pro Asp Ser Ile Arg Ile 335 340 345	1541
aag gtc gcg ctt gac gac ggc gag att acc ggg ttt aat gca aag gat Lys Val Ala Leu Asp Asp Gly Glu Ile Thr Gly Phe Asn Ala Lys Asp 350 355 360	1589
ttc tta atc tcc cat aaa aaa aga gac ttg ccg aag ccc aaa cta acg Phe Leu Ile Ser His Lys Lys Arg Asp Leu Pro Lys Pro Lys Leu Thr 365 370 375	1637
cct gaa aaa gcg aaa gca agc ctg aat ccc aac gta aaa gtt cag gag Pro Glu Lys Ala Lys Ala Ser Leu Asn Pro Asn Val Lys Val Gln Glu 380 385 390 395	1685
acg cgc ctt gct tta gtc acg aac gag ctt tcg caa gaa gtg ctc tgc Thr Arg Leu Ala Leu Val Thr Asn Glu Leu Ser Gln Glu Val Leu Cys 400 405 410	1733
tac gaa att ctc ggc acg att gaa aac gat aca ttc cgc atg ttc atc Tyr Glu Ile Leu Gly Thr Ile Glu Asn Asp Thr Phe Arg Met Phe Ile 415 420 425	1781
aat gcc aat gac ggc acg gaa gag aag gtt cag aaa atg aaa agc gca Asn Ala Asn Asp Gly Thr Glu Glu Lys Val Gln Lys Met Lys Ser Ala 430 435 440	1829
gaa ccg ata tac aac gac ttg taaaaacgat agatcaaagg gaaaaggcga Glu Pro Ile Tyr Asn Asp Leu 445 450	1880
taacatgcct tttccttttt agcattcgga ataattcgcc ctaaactttt ccatactgaa	1940
catatggggcg gaacgtccgc cggtaaattg aaaatgcccc gggccataaa ttttccgggc	2000

10295.204.ST25.txt

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agcggaggaa taatatgaaa acaatcgaac gggtattatt taagatactc gtcgtacaga 2060
cggtcattttt aatcagcgtg cagcttctttt ttcatctctc caaggctgag ccttatctgt 2120
caaaggctcgt gcagtatgaa ggcgtgaaca acatgaaaat cggcgaatgg atcgagacat 2180
ttaagccgta attcacgcta aaatctcccc tttttcgcct aatacatgat acaatcctat 2240
aaggagtacc agatagcaag gagaggaatt atggaaaaga aattatgcat tgcaatagac 2300
ggccctgcgg cagccggaaa aagcacctg gcgaaaatcg tggccagaaa aaa 2353

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<210> 119
 <211> 450
 <212> PRT
 <213> Bacillus licheniformis

<400> 119

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Thr Ser Tyr Trp Gly Tyr Lys Glu His Gln Glu Lys Asp Ala Val Leu
20 25 30

Leu His Ala Glu Asn Asn Tyr Gln Arg Ala Phe His Asp Leu Thr Tyr
35 40 45

Gln Val Asp Gln Leu His Asp Lys Ile Gly Ser Thr Leu Ala Met Asn
50 55 60

Ser Lys Lys Thr Leu Ser Pro Ala Leu Ala Glu Val Trp Lys Thr Thr
65 70 75 80

Ser Glu Ala His Asn Asn Val Ser Gln Leu Pro Leu Thr Leu Met Pro
85 90 95

Phe Asn Lys Thr Glu Glu Phe Leu Ala Lys Val Gly Asp Phe Ser Tyr
100 105 110

Lys Ala Ala Val Arg Asp Leu Asp Lys Glu Pro Leu Asn Lys Lys Glu
115 120 125

Tyr Ala Ser Leu Asn Gln Leu Tyr Glu Asn Ser Lys Asp Ile Gln Asn
130 135 140

Glu Leu Arg Asn Val Gln His Leu Ile Ile Asp Lys Asn Leu Arg Trp
145 150 155 160

Met Asp Val Glu Leu Ala Leu Ala Ser Gly Gln Lys Gln Ser Asp Asn
165 170 175

Lys Ile Ile Asn Gly Phe Lys Thr Val Glu Lys Ser Ala Ser Ala Phe
180 185 190

10295.204.ST25.txt

Ser Asp Thr Asp Leu Gly Ala Thr Glu Met Thr Asn Thr Lys Lys Glu
 195 200 205

Gln Gln Gly Tyr Asp His Leu Gln Gly Lys Arg Ile Thr Glu Lys Glu
 210 215 220

Ala Arg Lys Ile Ala Gln Lys Phe Ala Gln Asp Lys Asn Tyr Asn Ile
 225 230 235 240

Lys Val Ser Lys Ser Gly Lys Lys Thr Asn Arg Asp Val Tyr Ser Ile
 245 250 255

Ser Met Gln Asp Pro Asp Gln Lys Ala Asp Ile Tyr Met Asp Ile Thr
 260 265 270

Glu Lys Gly Gly Tyr Pro Val Tyr Leu Ile Gln Asn Lys Lys Ile Lys
 275 280 285

Asp Glu Lys Ile Ser Leu Asn Asp Ala Ser Asn Lys Ala Leu Gln Phe
 290 295 300

Leu Lys Lys Asn Gly Tyr Lys Thr Glu Asp Leu Lys Met Asp Glu Ser
 305 310 315 320

Ser Gln Tyr Asp Gly Val Gly Val Phe Ser Phe Val Pro Val Gln Asp
 325 330 335

Asp Val Trp Leu Tyr Pro Asp Ser Ile Arg Ile Lys Val Ala Leu Asp
 340 345 350

Asp Gly Glu Ile Thr Gly Phe Asn Ala Lys Asp Phe Leu Ile Ser His
 355 360 365

Lys Lys Arg Asp Leu Pro Lys Pro Lys Leu Thr Pro Glu Lys Ala Lys
 370 375 380

Ala Ser Leu Asn Pro Asn Val Lys Val Gln Glu Thr Arg Leu Ala Leu
 385 390 395 400

Val Thr Asn Glu Leu Ser Gln Glu Val Leu Cys Tyr Glu Ile Leu Gly
 405 410 415

Thr Ile Glu Asn Asp Thr Phe Arg Met Phe Ile Asn Ala Asn Asp Gly
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<213> Bacillus licheniformis
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 aaa ggc gag ccg ctc gtc acg gtg aac cag cac gtt gaa aaa ggg caa 914
 Lys Gly Glu Pro Leu Val Thr Val Asn Gln His Val Glu Lys Gly Gln
 210 215 220
 atg ctc gtt tcc ggg ctg atc gga agc gaa gag gaa aag caa aaa gtc 962
 Met Leu Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys Gln Lys Val
 225 230 235
 gga gca aaa ggg aaa atc tat ggt gaa acc tgg tac aag tca aca gta 1010
 Gly Ala Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys Ser Thr Val
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 Thr Val Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly Lys Val Arg
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 Thr Ser His Lys Leu Ser Leu Gly Ser Leu Thr Met Pro Ile Trp Gly
 275 280 285
 ttt tca ttt aaa aaa gaa gac ttc tcg cgc ccg aag acg gag acc gaa 1154
 Phe Ser Phe Lys Lys Glu Asp Phe Ser Arg Pro Lys Thr Glu Thr Glu
 290 295 300
 aaa cac tcg ctg cat ttt ata aat ttt aag ctt cct gtc gct tat gaa 1202
 Lys His Ser Leu His Phe Ile Asn Phe Lys Leu Pro Val Ala Tyr Glu
 305 310 315
 aag gag cat atg agg gag agc gaa caa atc aaa agg gtg tac tcg aaa 1250
 Lys Glu His Met Arg Glu Ser Glu Gln Ile Lys Arg Val Tyr Ser Lys
 320 325 330
 aaa gaa gca gtt ctt aga agg aat cga aat ggg aaa aag aga cat cag 1298
 Lys Glu Ala Val Leu Arg Arg Asn Arg Asn Gly Lys Lys Arg His Gln
 335 340 345 350
 gac aaa aat cgg cag aga cgg gaa cat tat cag tgt aaa agt ttt gca 1346
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<211> 369

<212> PRT

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<400> 121

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 35 40 45

10295.204.ST25.txt

Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg Lys Val Ile Arg Gly
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Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys Gly Phe Pro Phe Leu
 65 70 75 80

Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr Phe Gly Val Ala Ala
 85 90 95

Phe Phe Ile Ile Met Phe Leu Leu Ser Asn Met Leu Trp Lys Ile Asp
 100 105 110

Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln Ile Arg Gln Gln Leu
 115 120 125

Asp Gln Ile Gly Val Lys Lys Gly Arg Phe Gln Phe Ser Met Leu Thr
 130 135 140

Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg Val Glu Asn Ile Thr
 145 150 155 160

Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu His Met Lys Val Val
 165 170 175

Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile Gly Pro Arg His Ile
 180 185 190

Val Ala Lys Lys Gly Ala Thr Ile Ser Lys Met Phe Val Glu Lys Gly
 195 200 205

Glu Pro Leu Val Thr Val Asn Gln His Val Glu Lys Gly Gln Met Leu
 210 215 220

Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys Gln Lys Val Gly Ala
 225 230 235 240

Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys Ser Thr Val Thr Val
 245 250 255

Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly Lys Val Arg Thr Ser
 260 265 270

His Lys Leu Ser Leu Gly Ser Leu Thr Met Pro Ile Trp Gly Phe Ser
 275 280 285

Phe Lys Lys Glu Asp Phe Ser Arg Pro Lys Thr Glu Thr Glu Lys His
 290 295 300

Ser Leu His Phe Ile Asn Phe Lys Leu Pro Val Ala Tyr Glu Lys Glu
 305 310 315 320

10295.204.ST25.txt

His Met Arg Glu Ser Glu Gln Ile Lys Arg Val Tyr Ser Lys Lys Glu
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 gaaccttggg gcggtcaaaa accaacaatgt ctataaaatc gaccctgtcg gcttctatatt 300
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 gaagaacttc cgccttgtca ggcggaagtt ttttttgcgc gcgaaaccgg ggtgaaccct 420
 cattgaaaaa gcgattttca agtgcaagcc gggagagttt ttaaacgagc attcctcata 480
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aag cag aat atg gaa aga ctg tct gac att ctg aac ata ccc gaa ccg 581
 Lys Gln Asn Met Glu Arg Leu Ser Asp Ile Leu Asn Ile Pro Glu Pro
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ctt tta atc agt gca aat gca aat gta tcc gcg gac gaa ctt tat ttt 629
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ccg gga gta tct ttt cat gca gga aaa aac gtt caa gca gca gaa aca 677
 Pro Gly Val Ser Phe His Ala Gly Lys Asn Val Gln Ala Ala Glu Thr
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tat gaa cag ctg caa tta ttg gcg aat caa tac acg ttt gaa gat gaa 725
 Tyr Glu Gln Leu Gln Leu Leu Ala Asn Gln Tyr Thr Phe Glu Asp Glu
 60 65 70 75

cag tgg ctg aca aaa aca gcc gtt tac gat tca gca gaa ctg aaa aag 773
 Gln Trp Leu Thr Lys Thr Ala Val Tyr Asp Ser Ala Glu Leu Lys Lys
 80 85 90

gaa att ggc aga ttg acg gaa tgc ttt ccg ttt gtt act tcc cgt atc 821
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Glu Ile Gly Arg Leu Thr Glu Cys Phe Pro Phe Val Thr Ser Arg Ile
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 atc ggc cgc tca agc atg ggc cag cct ata tat gaa ctg ctc ctt gga 869
 Ile Gly Arg Ser Ser Met Gly Gln Pro Ile Tyr Glu Leu Leu Leu Gly
 110 115 120
 gct gaa aat gcc gga aaa aga acg cat atg aat gcc tct ttt cat gcc 917
 Ala Glu Asn Ala Gly Lys Arg Thr His Met Asn Ala Ser Phe His Ala
 125 130 135
 aat gaa tgg atc acc act tct gtt ttg atg aaa tgg ctc aaa gaa tac 965
 Asn Glu Trp Ile Thr Thr Ser Val Leu Met Lys Trp Leu Lys Glu Tyr
 140 145 150 155
 tgt tat cat tta tgt aca ggc cag acc gct tta ggt ttt tcg ccg ctc 1013
 Cys Tyr His Leu Cys Thr Gly Gln Thr Ala Leu Gly Phe Ser Pro Leu
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 Asp Ile Phe Ser Ser Thr Lys Leu Ser Val Val Pro Ile Val Asn Pro
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 190 195 200
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 Arg Asp Tyr Pro Gly Asp Glu Pro Leu Thr Glu Pro Glu Ala Ala Ala
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 atg agg gat tta atc gca aac gag ccg cct gac ccg ctt gtg gcg ctt 1349
 Met Arg Asp Leu Ile Ala Asn Glu Pro Pro Asp Arg Leu Val Ala Leu
 270 275 280
 cac aca cag ggg gag gaa att tat tgg gga tac aag gga ttg gag cct 1397
 His Thr Gln Gly Glu Glu Ile Tyr Trp Gly Tyr Lys Gly Leu Glu Pro
 285 290 295
 cct gaa tca gct gat gtg atc caa aca ttt gag cgc ctg agc ggt tat 1445
 Pro Glu Ser Ala Asp Val Ile Gln Thr Phe Glu Arg Leu Ser Gly Tyr
 300 305 310 315
 aag ggc gtc aga tat ata gac agc tat gca gga ttt aga gat tgg ttt 1493
 Lys Gly Val Arg Tyr Ile Asp Ser Tyr Ala Gly Phe Arg Asp Trp Phe
 320 325 330
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 Ile His Tyr Tyr Gly Arg Glu Gly Tyr Thr Val Glu Leu Gly Lys Gly
 335 340 345
 aaa aat cct tta ccg ctg aaa caa ttt gac gat ata tat tgt aaa agc 1589
 Lys Asn Pro Leu Pro Leu Lys Gln Phe Asp Asp Ile Tyr Cys Lys Ser
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 gagtttcatt attgattatt gccgctctga tggccgtggc tgcggctggt tgcacgccgc 1755
 agcatcaaga aggatcaaaa agcgttcatc atgaggagcc ggaagggaaa agagaaagcg 1815
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 aaatcaaadc atatgatata tttaaaggga cgggcaaac gatctacaag acagatgaca 1995
 ggctgatagc gtcggaagtc aacagtgaag aaggcatgat tcttatccaa accgccggaa 2055
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Asn Ala Asn Val Ser Ala Asp Glu Leu Tyr Phe Pro Gly Val Ser Phe
 35 40 45

His Ala Gly Lys Asn Val Gln Ala Ala Glu Thr Tyr Glu Gln Leu Gln
 50 55 60

Leu Leu Ala Asn Gln Tyr Thr Phe Glu Asp Glu Gln Trp Leu Thr Lys
 65 70 75 80

Thr Ala Val Tyr Asp Ser Ala Glu Leu Lys Lys Glu Ile Gly Arg Leu
 85 90 95

Thr Glu Cys Phe Pro Phe Val Thr Ser Arg Ile Ile Gly Arg Ser Ser
 100 105 110

Met Gly Gln Pro Ile Tyr Glu Leu Leu Leu Gly Ala Glu Asn Ala Gly
 115 120 125

Lys Arg Thr His Met Asn Ala Ser Phe His Ala Asn Glu Trp Ile Thr
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Thr Ser Val Leu Met Lys Trp Leu Lys Glu Tyr Cys Tyr His Leu Cys
 145 150 155 160

10295.204.ST25.txt

Thr Gly Gln Thr Ala Leu Gly Phe Ser Pro Leu Asp Ile Phe Ser Ser
 165 170 175
 Thr Lys Leu Ser Val Val Pro Ile Val Asn Pro Asp Gly Val Asp Leu
 180 185 190
 Val Leu Asn Gly Pro Gly His Leu Gly Ile Ala Arg Glu Ala Leu Asp
 195 200 205
 Glu Met Asn Glu His Gln Pro Asp Phe Arg Glu Trp Lys Ala Asn Ile
 210 215 220
 Asn Gly Val Asp Leu Asn Asn Gln Phe Pro Ser Phe Trp Glu Ile Glu
 225 230 235 240
 Lys Gln Arg Lys Pro Pro Lys Ser Pro Ser Tyr Arg Asp Tyr Pro Gly
 245 250 255
 Asp Glu Pro Leu Thr Glu Pro Glu Ala Ala Ala Met Arg Asp Leu Ile
 260 265 270
 Ala Asn Glu Pro Pro Asp Arg Leu Val Ala Leu His Thr Gln Gly Glu
 275 280 285
 Glu Ile Tyr Trp Gly Tyr Lys Gly Leu Glu Pro Pro Glu Ser Ala Asp
 290 295 300
 Val Ile Gln Thr Phe Glu Arg Leu Ser Gly Tyr Lys Gly Val Arg Tyr
 305 310 315 320
 Ile Asp Ser Tyr Ala Gly Phe Arg Asp Trp Phe Ile His Tyr Tyr Gly
 325 330 335
 Arg Glu Gly Tyr Thr Val Glu Leu Gly Lys Gly Lys Asn Pro Leu Pro
 340 345 350
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 Ala Ser Cys Phe Phe Glu Ser
 370 375

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Leu	Lys	Glu	Ser	Gly	Tyr	Ile	Met	Gly	Arg	Lys	Trp	Asn	Asn	Ile	Lys			
				10					15					20				
gag	aag	aaa	gcg	tcc	aag	gat	gcg	aat	acg	agc	cga	atc	tac	gcg	aag			452
Glu	Lys	Lys	Ala	Ser	Lys	Asp	Ala	Asn	Thr	Ser	Arg	Ile	Tyr	Ala	Lys			
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Phe	Gly	Arg	Glu	Ile	Tyr	Val	Ala	Ala	Lys	Gln	Gly	Glu	Pro	Asp	Pro			
		40					45					50						
gaa	ctg	aac	cag	aac	ctg	aaa	ttc	gtg	ctt	gag	cg	gcc	aaa	aca	tac			548
Glu	Leu	Asn	Gln	Asn	Leu	Lys	Phe	Val	Leu	Glu	Arg	Ala	Lys	Thr	Tyr			
	55					60					65							
aat	gtc	ccg	aaa	gcg	att	att	gag	cg	gcg	atc	gaa	aaa	gcg	aag	ggc			596
Asn	Val	Pro	Lys	Ala	Ile	Ile	Glu	Arg	Ala	Ile	Glu	Lys	Ala	Lys	Gly			
	70				75					80					85			
ggc	tct	gag	gaa	aat	tac	gac	gag	ctg	cg	tat	gaa	ggc	ttc	gg	ccg			644
Gly	Ser	Glu	Glu	Asn	Tyr	Asp	Glu	Leu	Arg	Tyr	Glu	Gly	Phe	Gly	Pro			
				90					95					100				
aac	gga	gcg	atg	gtg	atc	gtt	gac	gcg	ttg	aca	aac	aac	gtc	aac	cg			692
Asn	Gly	Ala	Met	Val	Ile	Val	Asp	Ala	Leu	Thr	Asn	Asn	Val	Asn	Arg			
			105					110					115					
acg	gct	gcc	gat	gtg	cg	tcc	aca	ttt	ggc	aaa	aac	ggc	gga	aac	atg			740
Thr	Ala	Ala	Asp	Val	Arg	Ser	Thr	Phe	Gly	Lys	Asn	Gly	Gly	Asn	Met			
		120					125					130						
gga	gtg	agc	gga	tct	gtc	gct	tac	atg	ttt	gat	ccg	acg	gcc	gtc	atc			788
Gly	Val	Ser	Gly	Ser	Val	Ala	Tyr	Met	Phe	Asp	Pro	Thr	Ala	Val	Ile			
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10295.204.ST25.txt

215 220 225 1076
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 230 235 240 245
 aat gtc gat tta ggg gcg taaaaagagg ccctgaaaaa atcgggaaag 1124
 Asn Val Asp Leu Gly Ala 250
 aaaagataga tgaacaggag gacgacctgt tttgtctatc tttttttatt gtaaagttaa 1184
 cttgacattt tttttttttg ttaagtatac tttagctata gtgaacttta cattcccaat 1244
 ggaggaaaga tgaacacgtt aataaaggaa aagcgcactt cgctgaacat gacacaagaa 1304
 gaactggcta aaaggcttaa tgtgtcgagg caaacggtga tttcccttga aaagggaaaa 1364
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 cgcttttagcg ggcttagaat aggcgtgctc gggatcgcaa ttgtttacaa agtaaacaga 1544
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 35 40 45

Gly Glu Pro Asp Pro Glu Leu Asn Gln Asn Leu Lys Phe Val Leu Glu
 50 55 60

Arg Ala Lys Thr Tyr Asn Val Pro Lys Ala Ile Ile Glu Arg Ala Ile
 65 70 75 80

Glu Lys Ala Lys Gly Gly Ser Glu Glu Asn Tyr Asp Glu Leu Arg Tyr
 85 90 95

Glu Gly Phe Gly Pro Asn Gly Ala Met Val Ile Val Asp Ala Leu Thr
 100 105 110

Asn Asn Val Asn Arg Thr Ala Ala Asp Val Arg Ser Thr Phe Gly Lys
 115 120 125

Asn Gly Gly Asn Met Gly Val Ser Gly Ser Val Ala Tyr Met Phe Asp
 130 135 140

10295.204.ST25.txt

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Glu Leu Leu Met Glu Ala Asp Ile Asp Val Arg Asp Ile Leu Glu Glu
165 170 175

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180 185 190

Gln Glu Ala Leu Gln Asn Ala Gly Ile Thr Glu Phe Thr Val Ala Glu
195 200 205

Leu Thr Met Leu Ala Gln Asn Asp Val Ala Leu Pro Glu Asp Ala Arg
210 215 220

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Gln Gln Val Tyr His Asn Val Asp Leu Gly Ala
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Ile Ala Phe Ser Ile Leu Tyr Leu Ser Ala Pro Phe Phe Ala Glu Met 30
20 25

gcc ctt ggc gga aca gaa aac aac ggg ctg acg ctt gaa cat gtc gtg 143
Ala Leu Gly Gly Thr Glu Asn Asn Gly Leu Thr Leu Glu His Val Val 45
35 40

tat gtc att cgc atg gtc agt ctc gcg cta ctg gtt gtg ccg atc ttg 191
Tyr Val Ile Arg Met Val Ser Leu Ala Leu Leu Val Val Pro Ile Leu 60
50 55

gcg ctg atc aga ggc ttt ttc caa ggt cac cag atg atg ggg ccg aca 239
Ala Leu Ile Arg Gly Phe Phe Gln Gly His Gln Met Met Gly Pro Thr 75
65 70

gcc gtt tca cag gta gtt gaa caa att gcc aga atc gtc ttt cta tta 287
Ala Val Ser Gln Val Val Glu Gln Ile Ala Arg Ile Val Phe Leu Leu 95
80 85 90

acg gcc act tac ttg gtg atc aaa gta tta aac ggc ggg ctt gtc gtc 335
Thr Ala Thr Tyr Leu Val Ile Lys Val Leu Asn Gly Gly Leu Val Val 110
100 105

10295.204.ST25.txt

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gcg ctg aag ccg aac ctt gtt cct tca gcc gat att acg tac cgg caa Ala Leu 145 Lys Pro Asn Leu Val 150 Pro Ser Ala Asp Ile 155 Thr Tyr Arg Gln	479
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gcg atg att gca gcc ggc tat caa aac atc agc cag gat ttg atg gcg Ala Met Ile 195 Ala Ala Gly Tyr Gln Asn 200 Ile Ser Gln Asp Leu Met Ala 205	623
atc gtg acg ctg tac gtg cca aag ctt gtg atg att ccg gta tct ctc Ile Val Thr 210 Leu Tyr Val Pro Lys Leu Val Met Ile Pro Val Ser Leu 220	671
gcg acg gca ttc ggg ctg aca ttg att ccg gcg gtg act gaa aac ttt Ala Thr 225 Ala Phe Gly Leu Thr 230 Leu Ile Pro Ala Val Thr Glu Asn Phe 235	719
acc aac aaa gat ttc cct gct tta aac aaa cag att gat cag gcg atg Thr Asn Lys Asp Phe 245 Pro Ala Leu Asn Lys Gln Ile Asp Gln Ala Met 255	767
cag atc att ctc ttc atc gtt ctt ccg gca tca gtc ggt atg gct ctt Gln Ile Ile Leu Phe 260 Ile Val Leu Pro Ala Ser Val Gly Met Ala Leu 270	815
ttg tcg ggg ccg gtt tac acg ttc ttt tac ggc tcg gaa agc ctg ctc Leu Ser Gly Pro Val Tyr Thr Phe 280 Tyr Gly Ser Glu Ser Leu Leu 285	863
cct gac atg gga cga gat att ttg ttc tgg tac gcg cct gtg gcg ctg Pro Asp Met Gly Arg Asp Ile Leu Phe Trp Tyr Ala Pro Val Ala Leu 300	911
tta ttc tcg ctc ttc acc gtc aac gct gca att ttg cag ggg gtg aac Leu Phe Ser Leu Phe Thr Val 310 Asn Ala Ala Ile Leu Gln Gly Val Asn 315	959
aag cag aaa ttt gcg gtt gtc agc ttg atg atc ggg att gtg atc aaa Lys Gln Lys Phe Ala Val 325 Val Ser Leu Met Ile Gly Ile Val Ile Lys 335	1007
atc gcg ctt aac gtt ccg ctc atc aag ctg ctt caa ggc agc ggg tcg Ile Ala Leu Asn Val 340 Pro Leu Ile Lys Leu Leu Gln Gly Ser Gly Ser 350	1055
att ttg gca acg gcg ctc ggc tat tca gct tca ctc cta tac gga ttt Ile Leu Ala Thr 355 Ala Leu Gly Tyr Ser Ala Ser Leu Leu Tyr Gly Phe 365	1103
atc atg att aaa cgc cat gcc ggc tat tcg tat cgc aaa ctg ttt aaa Ile Met Ile Lys Arg His Ala Gly Tyr Ser Tyr Arg Lys Leu Phe Lys 380	1151

10295.204.ST25.txt

cgg ttt ttg ctg atg ctg atc ctg acg gcg gtc atg ggc atc att ttg 1199
 Arg Phe Leu Leu Met Leu Ile Leu Thr Ala Val Met Gly Ile Ile Leu
 385 390

ctg ctt gtc cag gcg ctt cta agt att ttt att tca tac gaa ggc ggg 1247
 Leu Leu Val Gln Ala Leu Leu Ser Ile Phe Ile Ser Tyr Glu Gly Gly
 400 405 410 415

cag atc agg tct gct gtc gtc att ttc atc aca acc gca gtg ggc ggg 1295
 Gln Ile Arg Ser Ala Val Val Ile Phe Ile Thr Thr Ala Val Gly Gly
 420 425 430

tca gtt tat ctg tac ttg gct tac cgt gtg aaa ctg ctc gaa aaa atc 1343
 Ser Val Tyr Leu Tyr Leu Ala Tyr Arg Val Lys Leu Leu Glu Lys Ile
 435 440 445

ttc ggt cag cga ttg aat cgc ttt ttc aaa aga aag gcc tcc 1385
 Phe Gly Gln Arg Leu Asn Arg Phe Phe Lys Arg Lys Ala Ser
 450 455 460

taaaaagggc ttttcttttt atgtaaaaaa aggggtgtct tcatgagatt ggataaactg 1445
 ttgtcaaaca gcggctatgg ttcgagaaaa gaagtcaaaa aaatgctgaa aaacggcgcg 1505
 gtgcgcgtca atgatcaatt agtcaaagac gccaaaaagc acgttgaccc ggaatcagac 1565
 gacatcacgg tatacggggc acccgtcattg taccgggaat ttatttactt aatgatgaac 1625
 aagccgcaag gagtgctgtc agcaacagaa gacagccggc aggaaacggt tgtcgatttg 1685
 ctcgacccgg agctgctgag gtttgagccg tttcctgtcg gaaggcttga caaggatact 1745
 gagggactgc tgcttctgac gaatgacgga cagttggcac accagctttt atctccgaaa 1805
 aaacacgtac ctaaaacgta tgaagtccat gtcaataagc cgattgatca agcggcactt 1865
 gatcagcttg aaaaaggggt cga 1888

<210> 127
 <211> 461
 <212> PRT
 <213> Bacillus licheniformis

<400> 127

Lys Asp Ala Ala Arg Arg Asn Val Asp Asp Ala Arg Thr Gly Ile Ile
 1 5 10 15

Ala Phe Ser Ile Leu Tyr Leu Ser Ala Pro Phe Phe Ala Glu Met Ala
 20 25 30

Leu Gly Gly Thr Glu Asn Asn Gly Leu Thr Leu Glu His Val Val Tyr
 35 40 45

Val Ile Arg Met Val Ser Leu Ala Leu Leu Val Val Pro Ile Leu Ala
 50 55 60

Leu Ile Arg Gly Phe Phe Gln Gly His Gln Met Met Gly Pro Thr Ala
 65 70 75 80

Val Ser Gln Val Val Glu Gln Ile Ala Arg Ile Val Phe Leu Leu Thr
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85

90

95

Ala Thr Tyr Leu Val Ile Lys Val Leu Asn Gly Gly Leu Val Val Ala
 100 105 110

Val Gly Tyr Ala Thr Phe Ala Ala Leu Ile Gly Ala Phe Ala Gly Leu
 115 120 125

Phe Thr Leu Tyr Phe Ser Trp Gln Lys Arg Lys Gly Ala Leu Leu Ala
 130 135 140

Leu Lys Pro Asn Leu Val Pro Ser Ala Asp Ile Thr Tyr Arg Gln Met
 145 150 155 160

Phe Lys Glu Leu Phe Ser Tyr Ala Ala Pro Tyr Val Phe Val Gly Leu
 165 170 175

Ala Ile Pro Leu Tyr Gln Tyr Ile Asp Thr Asn Thr Phe Asn Lys Ala
 180 185 190

Met Ile Ala Ala Gly Tyr Gln Asn Ile Ser Gln Asp Leu Met Ala Ile
 195 200 205

Val Thr Leu Tyr Val Pro Lys Leu Val Met Ile Pro Val Ser Leu Ala
 210 215 220

Thr Ala Phe Gly Leu Thr Leu Ile Pro Ala Val Thr Glu Asn Phe Thr
 225 230 235 240

Asn Lys Asp Phe Pro Ala Leu Asn Lys Gln Ile Asp Gln Ala Met Gln
 245 250 255

Ile Ile Leu Phe Ile Val Leu Pro Ala Ser Val Gly Met Ala Leu Leu
 260 265 270

Ser Gly Pro Val Tyr Thr Phe Phe Tyr Gly Ser Glu Ser Leu Leu Pro
 275 280 285

Asp Met Gly Arg Asp Ile Leu Phe Trp Tyr Ala Pro Val Ala Leu Leu
 290 295 300

Phe Ser Leu Phe Thr Val Asn Ala Ala Ile Leu Gln Gly Val Asn Lys
 305 310 315 320

Gln Lys Phe Ala Val Val Ser Leu Met Ile Gly Ile Val Ile Lys Ile
 325 330 335

Ala Leu Asn Val Pro Leu Ile Lys Leu Leu Gln Gly Ser Gly Ser Ile
 340 345 350

Leu Ala Thr Ala Leu Gly Tyr Ser Ala Ser Leu Leu Tyr Gly Phe Ile
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355

360

365

Met Ile Lys Arg His Ala Gly Tyr Ser Tyr Arg Lys Leu Phe Lys Arg
 370 375 380

Phe Leu Leu Met Leu Ile Leu Thr Ala Val Met Gly Ile Ile Leu Leu
 385 390 395 400

Leu Val Gln Ala Leu Leu Ser Ile Phe Ile Ser Tyr Glu Gly Gly Gln
 405 410 415

Ile Arg Ser Ala Val Val Ile Phe Ile Thr Thr Ala Val Gly Gly Ser
 420 425 430

Val Tyr Leu Tyr Leu Ala Tyr Arg Val Lys Leu Leu Glu Lys Ile Phe
 435 440 445

Gly Gln Arg Leu Asn Arg Phe Phe Lys Arg Lys Ala Ser
 450 455 460

<210> 128
 <211> 1852
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1349)

<400> 128
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 ccgcgcggaa acattcggaa gatcgaaaga ccacagagaa agctatgacg ttgtgacggc 120
 acgcgctgtc gcccgccttt cggttctcag cgagctctgc cttccgcttg tgaaaaaaga 180
 cggttttattc gtagcattaa aagccgcttc ggctgatgaa gaaattgaaa cgggcaaaaa 240
 agccatcaaaa acgcttggag gcaaaattga aaccgtacat tcttttcagc tgccaataga 300
 agaaagcgaa agaaacatca ttgtcatcaa aaaacaatcg cagacaccga agaaatttcc 360
 aagaaagcct ggaacaccta ataaatctcc tattgaagggt taaattattc gttttcttca 420
 aatttcgtga tgtcacagaa ggaaaattca tgagaaaata gaattataaa aatggcagtg 480
 tttaaagggtg gtgtaggtac atg aag cat tca ttc tct cgt ctc ttc gga ctt 533
 Met Lys His Ser Phe Ser Arg Leu Phe Gly Leu
 1 5 10

ggc gac aag gaa gaa gaa gca gag att gct gaa cat gat acg aat aaa 581
 Gly Asp Lys Glu Glu Glu Ala Glu Ile Ala Glu His Asp Thr Asn Lys
 15 20 25

gaa gaa att caa gag att cca gta ggc gat ata att cct aac cgt ttt 629
 Glu Glu Ile Gln Glu Ile Pro Val Gly Asp Ile Ile Pro Asn Arg Phe
 30 35 40

cag ccg cgc acc att ttc tca gaa gaa aaa att aaa gaa tta gct gca 677
 Gln Pro Arg Thr Ile Phe Ser Glu Glu Lys Ile Lys Glu Leu Ala Ala

10295.204.ST25.txt

55

45 50 55
 acc att cat aca cac ggc att atc cag ccg att gtc gtc aga aaa aca 725
 Thr Ile His Thr His Gly Ile Ile Gln Pro Ile Val Val Arg Lys Thr 75
 60
 gag cgg gaa ggc caa tat gaa ctc ata gcc gga gag cgg cgc tgg cgg 773
 Glu Arg Glu Gly Gln Tyr Glu Leu Ile Ala Gly Glu Arg Arg Trp Arg 90
 80
 gcg gtt caa acg ctc gat tgg gag aag gtt ccc gct att att aag gat 821
 Ala Val Gln Thr Leu Asp Trp Glu Lys Val Pro Ala Ile Ile Lys Asp 105
 95
 ttt tca gat aca gag acc gct tct gtc gct ctt atc gaa aac ctt cag 869
 Phe Ser Asp Thr Glu Thr Ala Ser Val Ala Leu Ile Glu Asn Leu Gln 120
 110
 agg gaa gaa tta tct tcg att gaa gag gcg cat gct tat gca agg ctt 917
 Arg Glu Glu Leu Ser Ser Ile Glu Glu Ala His Ala Tyr Ala Arg Leu 135
 125
 tta gag ctt cac gat ttg acg cag gaa gcc ctt gca caa agg ctt gga 965
 Leu Glu Leu His Asp Leu Thr Gln Glu Ala Leu Ala Gln Arg Leu Gly 155
 140
 aag ggc cag tca aca atc gcc aat aag ctc aga ctg tta aag ctt ccg 1013
 Lys Gly Gln Ser Thr Ile Ala Asn Lys Leu Arg Leu Leu Lys Leu Pro 170
 160
 gaa gag gtg cag gaa gcg atc ttg aaa aaa gaa att tca gag cgc cac 1061
 Glu Glu Val Gln Glu Ala Ile Leu Lys Lys Glu Ile Ser Glu Arg His 185
 175
 gca aga gcg ctc ata ccg ttg aaa cag ccc gac ctt cag gtc aag ctg 1109
 Ala Arg Ala Leu Ile Pro Leu Lys Gln Pro Asp Leu Gln Val Lys Leu 200
 190
 ctg cat gaa gtc att gaa aag agt tta aat gta aaa caa acc gaa gac 1157
 Leu His Glu Val Ile Glu Lys Ser Leu Asn Val Lys Gln Thr Glu Asp 215
 205
 cgt gtc gtc aaa atg ctt gag cag gat aaa cgc aag cct aaa cca aag 1205
 Arg Val Val Lys Met Leu Glu Gln Asp Lys Arg Lys Pro Lys Pro Lys 235
 220
 aga aaa gcg tac agc agg gac gcg aga atc gcg atg aat acg att cgc 1253
 Arg Lys Ala Tyr Ser Arg Asp Ala Arg Ile Ala Met Asn Thr Ile Arg 250
 240
 cag tcc tta tca atg gtg gaa gac agc ggc gtc aaa ctg aat acg gaa 1301
 Gln Ser Leu Ser Met Val Glu Asp Ser Gly Val Lys Leu Asn Thr Glu 265
 255
 gaa gag gaa ttt gaa gaa tat att cag ttt acg att cga ata ccg aaa 1349
 Glu Glu Glu Phe Glu Glu Tyr Ile Gln Phe Thr Ile Arg Ile Pro Lys 280
 270
 taaaagctcc ctatagagct tttatttttt taggcaaaat atctatgggg gagcgtctat 1409
 ggaatattat cgacaatatc attcattgct tttttcgatt gcttaccgta tgctcggggtc 1469
 ttttcaagat gcagaggaca tcatccaaga attgttcgca gaccttcagg aaaaagatat 1529
 cgggtcaaatt gaccatattc aagcatattt aacgaaatca atcacaacc gctgcataaa 1589
 tgaactgcag tctgccccgca agaagcgggg ggtatatatc ggggaatggc ttccggaacc 1649

10295.204.ST25.txt

gcaggtggcg ctttcagctc aaatcccggc tgagtacgtt gaagagaaag aaaaggatc 1709
 ctatgctttt ctggtagtta tgagccgatt aaatcctgta gaaagagccg ttttgatgtt 1769
 tagagaagta tttggatatc attacaagga aatttcgtcc attatcgga agtcggaagc 1829
 gaactgtcgt caaatccaca gcc 1852

<210> 129
 <211> 283
 <212> PRT
 <213> Bacillus licheniformis

<400> 129

Met Lys His Ser Phe Ser Arg Leu Phe Gly Leu Gly Asp Lys Glu Glu
 1 5 10 15

Glu Ala Glu Ile Ala Glu His Asp Thr Asn Lys Glu Glu Ile Gln Glu
 20 25 30

Ile Pro Val Gly Asp Ile Ile Pro Asn Arg Phe Gln Pro Arg Thr Ile
 35 40 45

Phe Ser Glu Glu Lys Ile Lys Glu Leu Ala Ala Thr Ile His Thr His
 50 55 60

Gly Ile Ile Gln Pro Ile Val Val Arg Lys Thr Glu Arg Glu Gly Gln
 65 70 75 80

Tyr Glu Leu Ile Ala Gly Glu Arg Arg Trp Arg Ala Val Gln Thr Leu
 85 90 95

Asp Trp Glu Lys Val Pro Ala Ile Ile Lys Asp Phe Ser Asp Thr Glu
 100 105 110

Thr Ala Ser Val Ala Leu Ile Glu Asn Leu Gln Arg Glu Glu Leu Ser
 115 120 125

Ser Ile Glu Glu Ala His Ala Tyr Ala Arg Leu Leu Glu Leu His Asp
 130 135 140

Leu Thr Gln Glu Ala Leu Ala Gln Arg Leu Gly Lys Gly Gln Ser Thr
 145 150 155 160

Ile Ala Asn Lys Leu Arg Leu Leu Lys Leu Pro Glu Glu Val Gln Glu
 165 170 175

Ala Ile Leu Lys Lys Glu Ile Ser Glu Arg His Ala Arg Ala Leu Ile
 180 185 190

Pro Leu Lys Gln Pro Asp Leu Gln Val Lys Leu Leu His Glu Val Ile
 195 200 205

10295.204.ST25.txt

Glu Lys Ser Leu Asn Val Lys Gln Thr Glu Asp Arg Val Val Lys Met
 210 215 220

Leu Glu Gln Asp Lys Arg Lys Pro Lys Pro Lys Arg Lys Ala Tyr Ser
 225 230 235 240

Arg Asp Ala Arg Ile Ala Met Asn Thr Ile Arg Gln Ser Leu Ser Met
 245 250 255

Val Glu Asp Ser Gly Val Lys Leu Asn Thr Glu Glu Glu Glu Phe Glu
 260 265 270

Glu Tyr Ile Gln Phe Thr Ile Arg Ile Pro Lys
 275 280

<210> 130
 <211> 1495
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(995)

<400> 130
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 tcgtccatga gcctgatgcc gctttaacgg caaatcaata ccccgatcaat ctgcaaatat 120
 ccggacacac ccacgcgcgg acaaattcag attcctgtat tcggtccttt gattacgcct 180
 ccgtacgtag acgtttatac gcaaggaatg tatgcaacag ccggaatgaa aatttatgtc 240
 atttgaggaa tcggcacgag caggctgccc ctccgctttc tgtcaaagcc tgaaatcacc 300
 gtgttccagc ttgaatccat ttaattcttg ccggtccttt ggctcaaaac aaaaggcatc 360
 tgcatacatt aagtaaaaac attcccgtc catttcatcc aatcccatca aaaaaacgga 420
 acttcctcag cctcttccgt ctatatatta gcagcggaaa aggcctctctt ttcgtttttg 480
 aaaaggagat gtgctgatta ttg ctg atg tac caa gtc aaa ccc gga gga acc 533
 1 5 10
 Leu Leu Met Tyr Gln Val Lys Pro Gly Gly Thr
 ctt gaa agc atc gcc gcc gat ttc aga acg acc cgg cag gcg ttg ctg 581
 Leu Glu Ser Ile Ala Ala Asp Phe Arg Thr Thr Arg Gln Ala Leu Leu
 15 20 25
 cag gcg aat cct ggc tta aac ggc ggc caa gtg tcc gcg ggc cag tcg 629
 Gln Ala Asn Pro Gly Leu Asn Gly Gly Gln Val Ser Ala Gly Gln Ser
 30 35 40
 att atc att ccc ggc atc aga aat ccg gac aca att cca tac cgg att 677
 Ile Ile Ile Pro Gly Ile Arg Asn Pro Asp Thr Ile Pro Tyr Arg Ile
 45 50 55
 gcc gtg tct ctc aac gga aga acg ctc aga ttg tat gag cga gac aga 725
 Ala Val Ser Leu Asn Gly Arg Thr Leu Arg Leu Tyr Glu Arg Asp Arg
 60 65 70 75
 ctt gta aaa aca tat ccg att gcc gtc gga aaa atc ctc aca cag acg 773
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Leu Val Lys Thr Tyr Pro Ile Ala Val Gly Lys Ile Leu Thr Gln Thr
 80 85 90
 ccg aga ggc gaa ttt gtc atc gtc aac cgg cag cca aat ccg ggc ggc 821
 Pro Arg Gly Glu Phe Val Ile Val Asn Arg Gln Pro Asn Pro Gly Gly
 95 100 105
 ccg ttc ggc gcc tac tgg ctg agc ctg tca aaa cag cac tac ggc atc 869
 Pro Phe Gly Ala Tyr Trp Leu Ser Leu Ser Lys Gln His Tyr Gly Ile
 110 115 120
 cat gga acg aat aac cct tcg tca att ggc aaa gct gtt tca agg gga 917
 His Gly Thr Asn Asn Pro Ser Ser Ile Gly Lys Ala Val Ser Arg Gly
 125 130 135
 tgt atc cgc atg cac aat cgg gat gtt ctg gaa ctt gct tct atc gta 965
 Cys Ile Arg Met His Asn Arg Asp Val Leu Glu Leu Ala Ser Ile Val
 140 145 150 155
 ccc aac gga acc cga gtg tcc att aca cct tagacgagta catttccaga 1015
 Pro Asn Gly Thr Arg Val Ser Ile Thr Pro
 160 165
 caaatgcaat ttgaacaata caacatcttg tattaagata taatgggacc tttagggttaa 1075
 ggagcgtata tatggatctt tttaaaaatc gtaatttcgt cgcacttttt ttcgcagctt 1135
 tcgcttctca aatgggaacg acagtcggaa atatggcttt cgcctttttc ttgctcgacc 1195
 ggttcagcag ccagccggcc tatacgacaa tcgccgagct gatgtattcc ttgccgacgg 1255
 ttttcgtatt ctttatcgtc ggggtggctg ctgaccgttt tgaccgcaag aaagtcgcgg 1315
 aaaactgtga ttggatcaga ggccgggactg actgtcgttc ttttctttgt attgtatctt 1375
 caaattatac cgcttgtgtt tttagtccta tttatcagaa gcgcgggttac aaaatttttc 1435
 taccgggccg aagcaagttt ggtccaggcc attttaagaa aggaccagta tgcaaaggct 1495
 <210> 131
 <211> 165
 <212> PRT
 <213> Bacillus licheniformis
 <400> 131

Leu Leu Met Tyr Gln Val Lys Pro Gly Gly Thr Leu Glu Ser Ile Ala
 1 5 10 15

Ala Asp Phe Arg Thr Thr Arg Gln Ala Leu Leu Gln Ala Asn Pro Gly
 20 25 30

Leu Asn Gly Gly Gln Val Ser Ala Gly Gln Ser Ile Ile Ile Pro Gly
 35 40 45

Ile Arg Asn Pro Asp Thr Ile Pro Tyr Arg Ile Ala Val Ser Leu Asn
 50 55 60

Gly Arg Thr Leu Arg Leu Tyr Glu Arg Asp Arg Leu Val Lys Thr Tyr
 65 70 75 80

Pro Ile Ala Val Gly Lys Ile Leu Thr Gln Thr Pro Arg Gly Glu Phe
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10295.204.ST25.txt

85

90

95

Val Ile Val Asn Arg Gln Pro Asn Pro Gly Gly Pro Phe Gly Ala Tyr
 100 105 110

Trp Leu Ser Leu Ser Lys Gln His Tyr Gly Ile His Gly Thr Asn Asn
 115 120 125

Pro Ser Ser Ile Gly Lys Ala Val Ser Arg Gly Cys Ile Arg Met His
 130 135 140

Asn Arg Asp Val Leu Glu Leu Ala Ser Ile Val Pro Asn Gly Thr Arg
 145 150 155 160

Val Ser Ile Thr Pro
 165

<210> 132
 <211> 1897
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1397)

<400> 132
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 tatttgtccc tcagcctaac gtagattccg cggatcatcag gctgacgctg aggaaagagc 120
 cggctgtggc cgttcaagat gctgcctttt tctttcaagt cgtaaaagca agctttgcac 180
 agcgctcga aaacgcttttc aacaacctcg tcaacaatct gccgaatggc aaagagaata 240
 aatcaaaaat tgaaagagcg cttcaggatt cacatatcga cggaaaacga cgcgagagat 300
 cgcttagcat tgaagagtcc gccgtcttat ctgaccgctt gagagaagtc cttctttaat 360
 ggaggggcttt ttttattgat gccgggcttt aagcctgatc aggcttgta tccgttcacc 420
 acttgaaggg caggcacata ggctaaagaa gcacctttac ttttcgttg cttgatgttc 480
 atcaggatgg ggcttagtct atg tgt gga gtg aaa agc atg caa ttt aaa ata 533
 Met Cys Gly Val Lys Ser Met Gln Phe Lys Ile
 1 5 10

ggc gat atg gtc gtc aga aaa tct tat cga aga gat att tta ttt cga 581
 Gly Asp Met Val Val Arg Lys Ser Tyr Arg Arg Asp Ile Leu Phe Arg
 15 20 25

att ata aga att gat caa tcg gca aat gga gaa cct gta gcc gtt ttg 629
 Ile Ile Arg Ile Asp Gln Ser Ala Asn Gly Glu Pro Val Ala Val Leu
 30 35 40

cac gga gat gag gtc aga tta atc gct gac gcg cat ttg ggg gat ctt 677
 His Gly Asp Glu Val Arg Leu Ile Ala Asp Ala His Leu Gly Asp Leu
 45 50 55

gag att gtc cgc gag gct gag tgg cag atg aga aag cgg gaa gaa gaa 725
 Glu Ile Val Arg Glu Ala Glu Trp Gln Met Arg Lys Arg Glu Glu Glu
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60	65	70	75	
acg aga atg aag gaa tcc ctc gat ctt ctc cgc cag gat tac aaa ctc				773
Thr Arg Met Lys 80	Glu Ser Leu Asp Leu	Leu Arg Gln Asp Tyr Lys 90	Leu	
ctt cac gat aaa cat gag tac cgc gcc aca aac caa tat aac aat caa				821
Leu His Asp Lys 95	His Glu Tyr Arg Ala 100	Thr Asn Gln Tyr Asn Asn Gln 105		
cag cag tac ttt cat atg ccc gga aga gtc ctt cat tta gac ggg gat				869
Gln Gln Tyr 110	Phe His Met Pro Gly 115	Arg Val Leu His Leu Asp Gly Asp 120		
tcg gct tat ttg aaa aag tgt ctg gcg ctc tac gaa aag atc ggg gtt				917
Ser Ala Tyr 125	Leu Lys Lys Cys 130	Leu Ala Leu Tyr Glu Lys 135	Val	
cct gta tac ggc att cat tgc tat gaa aag aaa atg tca tca gtc atc				965
Pro Val Tyr 140	Gly Ile His Cys Tyr Glu Lys 145	Lys Met Ser Ser Val 150 155		
gag gaa ctg atc gat gaa tac cgc ccg gat ctt ctc gtc att acc gga				1013
Glu Glu Leu Ile 160	Asp Glu Tyr Arg Pro Asp 165	Leu Leu Val Ile Thr Gly 170		
cac gat gcc tat tct aag cag aag ggc gat att aac aat ctg gat gcc				1061
His Asp Ala Tyr 175	Ser Lys Gln Lys Gly Asp Ile Asn Asn Leu Asp Ala 185			
tac agg cat tca aaa gat ttt atc gaa acc gtt caa aaa gcg aga aga				1109
Tyr Arg His 190	Ser Lys Asp Phe Ile Glu Thr Val Gln Lys Ala Arg Arg 200			
aaa att ccc cat ctt gat cag ctc gtc att ttt gcc ggc gca tgc cag				1157
Lys Ile Pro 205	His Leu Asp Gln Leu Val Ile Phe Ala Gly Ala Cys Gln 215			
tcc cat ttt gaa tca ctg atc aga gcc ggt gca aat ttc gca agc tct				1205
Ser His Phe Glu Ser 220	Leu Ile Arg Ala Gly Ala Asn Phe Ala Ser Ser 225 235			
ccg tcc aga gtc aac atc cat gcg ctt gat ccg gtc tat ata gtc gca				1253
Pro Ser Arg Val 240	Asn Ile His Ala Leu Asp Pro Val Tyr Ile Val Ala 245 250			
aaa atc agc ttc act ccg ttt atg gac cgc att aac gtc tgg gaa gtg				1301
Lys Ile Ser Phe Thr 255	Pro Phe Met Asp Arg Ile Asn Val Trp Glu Val 265			
ctc aga aat acc ttg acg aga gaa aag ggg ctc gga ggt att gag acg				1349
Leu Arg Asn Thr 270	Leu Thr Arg Glu Lys Gly Leu Gly Ile Glu Thr 275 280			
cgg ggc gta ttg cgt att gga atg cca tat aaa aca aaa gca aac gat				1397
Arg Gly Val Leu Arg Ile 285	Gly Met Pro Tyr Lys Thr Lys Ala Asn Asp 295			
taaacgagcc cgccggatgg cgggtttttg ctatgcacac gaaatgtttt tacctttttt				1457
ttaaaaacat acataatgaa acgaaaaatg aggaaaataa gggaaagtcg gcgtataatt				1517
tgtcacaaat atttttattga cagaggctta tgaacgttga tataattttaa atttttattg				1577
acaaaaatgg gcttctgggtg tatactgaat atagtggagt ggatgcaatg gcgaaaacgt				1637
tgtccgatat taaaagatcg cttgatggac atttgggaaa aaggctgacg ttaaaagcaa				1697

10295.204.ST25.txt

acggtggccg ccgaaaaacg attgagcgtt cgggcatttt agctgagacg tacccttctg 1757
 tttttgtgat acaactagac caagacgaga attcgtttga aagagtttca tacagttatg 1817
 cggatattct tactgagacg gttgaattga ggttttccga tgataaaacc agctcagtag 1877
 ccctttaata agcagtggac 1897

<210> 133
 <211> 299
 <212> PRT
 <213> Bacillus licheniformis

<400> 133

Met Cys Gly Val Lys Ser Met Gln Phe Lys Ile Gly Asp Met Val Val
 1 5 10 15

Arg Lys Ser Tyr Arg Arg Asp Ile Leu Phe Arg Ile Ile Arg Ile Asp
 20 25 30

Gln Ser Ala Asn Gly Glu Pro Val Ala Val Leu His Gly Asp Glu Val
 35 40 45

Arg Leu Ile Ala Asp Ala His Leu Gly Asp Leu Glu Ile Val Arg Glu
 50 55 60

Ala Glu Trp Gln Met Arg Lys Arg Glu Glu Glu Thr Arg Met Lys Glu
 65 70 75 80

Ser Leu Asp Leu Leu Arg Gln Asp Tyr Lys Leu Leu His Asp Lys His
 85 90 95

Glu Tyr Arg Ala Thr Asn Gln Tyr Asn Asn Gln Gln Gln Tyr Phe His
 100 105 110

Met Pro Gly Arg Val Leu His Leu Asp Gly Asp Ser Ala Tyr Leu Lys
 115 120 125

Lys Cys Leu Ala Leu Tyr Glu Lys Ile Gly Val Pro Val Tyr Gly Ile
 130 135 140

His Cys Tyr Glu Lys Lys Met Ser Ser Val Ile Glu Glu Leu Ile Asp
 145 150 155 160

Glu Tyr Arg Pro Asp Leu Leu Val Ile Thr Gly His Asp Ala Tyr Ser
 165 170 175

Lys Gln Lys Gly Asp Ile Asn Asn Leu Asp Ala Tyr Arg His Ser Lys
 180 185 190

Asp Phe Ile Glu Thr Val Gln Lys Ala Arg Arg Lys Ile Pro His Leu
 195 200 205

10295.204.ST25.txt

Asp Gln Leu Val Ile Phe Ala Gly Ala Cys Gln Ser His Phe Glu Ser
 210 215 220

Leu Ile Arg Ala Gly Ala Asn Phe Ala Ser Ser Pro Ser Arg Val Asn
 225 230 235 240

Ile His Ala Leu Asp Pro Val Tyr Ile Val Ala Lys Ile Ser Phe Thr
 245 250 255

Pro Phe Met Asp Arg Ile Asn Val Trp Glu Val Leu Arg Asn Thr Leu
 260 265 270

Thr Arg Glu Lys Gly Leu Gly Gly Ile Glu Thr Arg Gly Val Leu Arg
 275 280 285

Ile Gly Met Pro Tyr Lys Thr Lys Ala Asn Asp
 290 295

<210> 134
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 <212> DNA
 <213> Bacillus licheniformis

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 <222> (501)..(734)

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 gctggaggtg attcaacatg aaaaaagcga aaaggcgaac atttgaagaa cttgtctcgg 180
 aaaataaaaa ggagctcatg accaaccagg agtttcttga tcggctggaa gataagcttg 240
 aagagaaatt taagctgaag tgagttttta aaaatcgatt catgtttacg ctcttttttg 300
 agaatcctaa tgctgaaaag gagggataga catgccgaga gaacacgaca aacagtctaa 360
 atttgccccg agccatcttg ggacaaaacc ggtagaatat aagcgcaaca aaggaaaaaa 420
 gatgcatgat aaatcaggag aaacaccgat cattatgcag acaaaaggcg agtaaagatg 480
 aaaaggaggc agagaccgga atg aca cat caa aaa cat cat ccg gat gac aga 533
 Met Thr His Gln Lys His His Pro Asp Asp Arg
 1 5 10

tca gac aac gta gaa aag ctt caa gac atg gtg cag aac aca atc gaa 581
 Ser Asp Asn Val Glu Lys Leu Gln Asp Met Val Gln Asn Thr Ile Glu
 15 20 25

aac att gag gag tct gaa gag cag ctg tct ttt gcc agc gag gcg gaa 629
 Asn Ile Glu Glu Ser Glu Glu Gln Leu Ser Phe Ala Ser Glu Ala Glu
 30 35 40

cag gaa cag atc cgc gaa aaa aat gaa cgc cga aat gaa agc att gag 677
 Gln Glu Gln Ile Arg Glu Lys Asn Glu Arg Arg Asn Glu Ser Ile Glu
 45 50 55

gcg atg cgc aat gaa atc cat gac gag gcg gaa gcc cgc aaa aac gga 725
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Ala Met Arg Asn Glu Ile His Asp Glu Ala Glu Ala Arg Lys Asn Gly
 60 65 70 75
 tat cat caa taaaccaggg cgacctgggt tttttgcatg aagcccgtcc 774
 Tyr His Gln

gtcgtgtttt tgcccattgt atatgctaga attggattaa atacatttgt ggaaaagggg 834
 gtagagggga aatttgtacg tctcaaaaaa agaaatagaa gtccgctatg ccgaaacaga 894
 cccaaaatgg ggtgtcgtct atcacgcaa ttatttgatt ttgggatggg aggtaagccc 954
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<210> 135
 <211> 78
 <212> PRT
 <213> Bacillus licheniformis

<400> 135

Met Thr His Gln Lys His His Pro Asp Asp Arg Ser Asp Asn Val Glu
 1 5 10 15

Lys Leu Gln Asp Met Val Gln Asn Thr Ile Glu Asn Ile Glu Glu Ser
 20 25 30

Glu Glu Gln Leu Ser Phe Ala Ser Glu Ala Glu Gln Glu Gln Ile Arg
 35 40 45

Glu Lys Asn Glu Arg Arg Asn Glu Ser Ile Glu Ala Met Arg Asn Glu
 50 55 60

Ile His Asp Glu Ala Glu Ala Arg Lys Asn Gly Tyr His Gln
 65 70 75

<210> 136
 <211> 2407
 <212> DNA
 <213> Bacillus licheniformis

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 <222> (501)..(1907)

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 aaaccttggc gtttcgatgg aaaacatccg ctatgagagc tttgcttcac ctcttgatat 180
 gcaaatagcg aactaacctc aagaaggcag ctgtcaaacc gacagctgcc tcagcgtgtc 240
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 ctccgctccg atgctcggcc ttcctagact gcaagggttt tcaatcacgc tgaaagaagg 360
 atgacaaaat cccaaaacta agagctgttt tgggattttg tcagcaatct aaggcagctg 420

10295.204.ST25.txt

tcaatccgac agctgccttt catcttttca aaacccggct catacaataa agagaagtcc	480
aaccggggggg gatttgagta ttg agc ata cgg gag caa aaa gag ctg cag cgg	533
Leu Ser Ile Arg Glu Gln Lys Glu Leu Gln Arg	10
1 5	
gcg att gaa gaa att acg gaa atc gcg gaa gga ttc ggc ctt gat ttt	581
Ala Ile Glu Glu Ile Thr Glu Ile Ala Glu Gly Phe Gly Leu Asp Phe	25
15 20	
tac ccg atg aga tat gag att tgt cct gct gaa att att tat aca ttc	629
Tyr Pro Met Arg Tyr Glu Ile Cys Pro Ala Glu Ile Ile Tyr Thr Phe	40
30 35	
ggt gca tac ggg atg ccg aca aga tac agc cat tgg agt ttc gga aag	677
Gly Ala Tyr Gly Met Pro Thr Arg Tyr Ser His Trp Ser Phe Gly Lys	55
45 50	
caa ttt cac aaa atg aag ctt cac tat gac ttt ggc ttg agc aaa ata	725
Gln Phe His Lys Met Lys Leu His Tyr Asp Phe Gly Leu Ser Lys Ile	75
60 65 70	
tat gag ctt gtc att aat tca gat ccg tgt tat gcg ttt ttg ctg gac	773
Tyr Glu Leu Val Ile Asn Ser Asp Pro Cys Tyr Ala Phe Leu Leu Asp	90
80 85	
agc aat tca ttg att caa aat aag ctg att gtc gca cac gtc ctt gct	821
Ser Asn Ser Leu Ile Gln Asn Lys Leu Ile Val Ala His Val Leu Ala	105
95 100	
cat tgt gat ttc ttt aaa aat aac tgc cgt ttt caa aat acg aag cgc	869
His Cys Asp Phe Phe Lys Asn Asn Cys Arg Phe Gln Asn Thr Lys Arg	120
110 115	
gat atg gtt gaa agc atg tcg gcg aca gca gag cgg att aaa cat tat	917
Asp Met Val Glu Ser Met Ser Ala Thr Ala Glu Arg Ile Lys His Tyr	135
125 130	
gaa acg gta cac ggt tca aaa gaa gtc gaa gca ttt ctc gat gcg gtg	965
Glu Thr Val His Gly Ser Lys Glu Val Glu Ala Phe Leu Asp Ala Val	155
140 145 150	
ctg gcg att gaa gaa cac att gac cct tcg ctc gtg agg ccg aag ctg	1013
Leu Ala Ile Glu Glu His Ile Asp Pro Ser Leu Val Arg Pro Lys Leu	170
160 165	
tcg tgg agc gta gat gat gaa gag gaa gaa gaa acc ggc gcg ccg gcc	1061
Ser Trp Ser Val Asp Asp Glu Glu Glu Glu Glu Thr Gly Ala Pro Ala	185
175 180	
act cct tat gac gac ctc tgg gaa ctg gat cat aaa gga tcg aaa gag	1109
Thr Pro Tyr Asp Asp Leu Trp Glu Leu Asp His Lys Gly Ser Lys Glu	200
190 195	
aag aag aaa agg acg aaa aaa aag ttt ccg ccg aaa ccg gaa aaa gac	1157
Lys Lys Lys Arg Thr Lys Lys Lys Phe Pro Pro Lys Pro Glu Lys Asp	215
205 210 215	
att ctg ctg ttc ata gaa gag cat tcg cgg gag ctg gag cct tgg cag	1205
Ile Leu Leu Phe Ile Glu Glu His Ser Arg Glu Leu Glu Pro Trp Gln	235
220 225 230	
cgc gat att tta acg atg atg aga gag gaa atg ctg tat ttc tgg ccg	1253
Arg Asp Ile Leu Thr Met Met Arg Glu Glu Met Leu Tyr Phe Trp Pro	250
240 245 250	
cag ctt gaa acg aaa atc atg aat gaa ggc tgg gcg tcc tat tgg cat	1301
Gln Leu Glu Thr Lys Ile Met Asn Glu Gly Trp Ala Ser Tyr Trp His	

10295.204.ST25.txt

255

260

265

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aat cct tat tat ctc gga ttg aaa ata ttt gag gac ata gag gag cgc Asn Pro Tyr Tyr Leu Gly Leu Lys Ile Phe Glu Asp Ile Glu Glu Arg 300 305 310 315	1445
tac aac aac ccg aca gaa gac atg aaa aag atg ggg gta gag ccg aac Tyr Asn Asn Pro Thr Glu Asp Met Lys Lys Met Gly Val Glu Pro Asn 320 325 330	1493
tct ggg aga gaa aaa ata ttt gaa gtc agg gag atc gaa tca gac att Ser Gly Arg Glu Lys Ile Phe Glu Val Arg Glu Ile Glu Ser Asp Ile 335 340 345	1541
tca ttt atc agg aac tat tta acg aag gat ctt gtg atg ccg gaa gac Ser Phe Ile Arg Asn Tyr Leu Thr Lys Asp Leu Val Met Arg Glu Asp 350 355 360	1589
ctc tac ttg ttt caa aaa cag gga agg gat tat aaa atc gtc gac aag Leu Tyr Leu Phe Gln Lys Gln Gly Arg Asp Tyr Lys Ile Val Asp Lys 365 370 375	1637
gat tgg gag gct gtg cgc gat cag ctt gtc agc atg aga gtc aac gga Asp Trp Glu Ala Val Arg Asp Gln Leu Val Ser Met Arg Val Asn Gly 380 385 390 395	1685
gga ttt cct tat ttg aca gtt gag gac gga gat tac tta aag aac aat Gly Phe Pro Tyr Leu Thr Val Glu Asp Gly Asp Tyr Leu Lys Asn Asn 400 405 410	1733
gaa tta tac atc aag cat tgg tat gaa ggg atc gaa ctc gat ttg aag Glu Leu Tyr Ile Lys His Trp Tyr Glu Gly Ile Glu Leu Asp Leu Lys 415 420 425	1781
tat ctt gaa aaa gtt ctg cct tac ctc cac cag cta tgg gga aga agc Tyr Leu Glu Lys Val Leu Pro Tyr Leu His Gln Leu Trp Gly Arg Ser 430 435 440	1829
gtg cat gtc gag acc gtg ctc gaa gat aaa ccc gtc atg ttt tcc tat Val His Val Glu Thr Val Leu Glu Asp Lys Pro Val Met Phe Ser Tyr 445 450 455	1877
gat gga aag gct gtc cac cgc aga tat tta taaaggctgc attttggcag Asp Gly Lys Ala Val His Arg Arg Tyr Leu 460 465	1927
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ttgaaaatat aaaatattct gctattggga ggacaacatg aaaaaacaag taataacagc	2347

10295.204.ST25.txt

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<210> 137
 <211> 469
 <212> PRT
 <213> Bacillus licheniformis

<400> 137

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 20 25 30

Glu Ile Cys Pro Ala Glu Ile Ile Tyr Thr Phe Gly Ala Tyr Gly Met
 35 40 45

Pro Thr Arg Tyr Ser His Trp Ser Phe Gly Lys Gln Phe His Lys Met
 50 55 60

Lys Leu His Tyr Asp Phe Gly Leu Ser Lys Ile Tyr Glu Leu Val Ile
 65 70 75 80

Asn Ser Asp Pro Cys Tyr Ala Phe Leu Leu Asp Ser Asn Ser Leu Ile
 85 90 95

Gln Asn Lys Leu Ile Val Ala His Val Leu Ala His Cys Asp Phe Phe
 100 105 110

Lys Asn Asn Cys Arg Phe Gln Asn Thr Lys Arg Asp Met Val Glu Ser
 115 120 125

Met Ser Ala Thr Ala Glu Arg Ile Lys His Tyr Glu Thr Val His Gly
 130 135 140

Ser Lys Glu Val Glu Ala Phe Leu Asp Ala Val Leu Ala Ile Glu Glu
 145 150 155 160

His Ile Asp Pro Ser Leu Val Arg Pro Lys Leu Ser Trp Ser Val Asp
 165 170 175

Asp Glu Glu Glu Glu Glu Thr Gly Ala Pro Ala Thr Pro Tyr Asp Asp
 180 185 190

Leu Trp Glu Leu Asp His Lys Gly Ser Lys Glu Lys Lys Lys Arg Thr
 195 200 205

Lys Lys Lys Phe Pro Pro Lys Pro Glu Lys Asp Ile Leu Leu Phe Ile
 210 215 220

Glu Glu His Ser Arg Glu Leu Glu Pro Trp Gln Arg Asp Ile Leu Thr
 225 230 235 240

10295.204.ST25.txt

Met Met Arg Glu Glu Met Leu Tyr Phe Trp Pro Gln Leu Glu Thr Lys
245 250 255

Ile Met Asn Glu Gly Trp Ala Ser Tyr Trp His Gln Arg Ile Ile Arg
260 265 270

Glu Leu Asp Leu Thr Ser Ser Glu Ala Ile Glu Phe Ala Lys Leu Asn
275 280 285

Ala Gly Val Val Gln Pro Ser Lys Thr Gly Ile Asn Pro Tyr Tyr Leu
290 295 300

Gly Leu Lys Ile Phe Glu Asp Ile Glu Glu Arg Tyr Asn Asn Pro Thr
305 310 315 320

Glu Asp Met Lys Lys Met Gly Val Glu Pro Asn Ser Gly Arg Glu Lys
325 330 335

Ile Phe Glu Val Arg Glu Ile Glu Ser Asp Ile Ser Phe Ile Arg Asn
340 345 350

Tyr Leu Thr Lys Asp Leu Val Met Arg Glu Asp Leu Tyr Leu Phe Gln
355 360 365

Lys Gln Gly Arg Asp Tyr Lys Ile Val Asp Lys Asp Trp Glu Ala Val
370 375 380

Arg Asp Gln Leu Val Ser Met Arg Val Asn Gly Gly Phe Pro Tyr Leu
385 390 395 400

Thr Val Glu Asp Gly Asp Tyr Leu Lys Asn Asn Glu Leu Tyr Ile Lys
405 410 415

His Trp Tyr Glu Gly Ile Glu Leu Asp Leu Lys Tyr Leu Glu Lys Val
420 425 430

Leu Pro Tyr Leu His Gln Leu Trp Gly Arg Ser Val His Val Glu Thr
435 440 445

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His Arg Arg Tyr Leu
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<210> 138
<211> 1291
<212> DNA
<213> Bacillus licheniformis

10295.204.ST25.txt

<220>

<221> CDS

<222> (501)..(791)

<400> 138

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gtgctgaaag aagcggggcgc ctctctggag actgtcgtca aagcaaccgt gtttctggcg      180
gatatgaatc aattcacaga ggtgaatgaa gtttacggac agtacttcga tacccacaaa      240
ccggcgagat catgcgttga ggtggcgagg ctgccgaaag acgcgcttgt tgaaatagaa      300
gtcatcgcat tagtgaaata gaaagaactc ttaaaagatg gttttggtct caaaatcatc      360
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ggaaaagggtg gtgaactact gtg gaa gtt acc gac gta aga tta cgc cgc gtg      533
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Asn Thr Asp Gly Arg Met Arg Ala Ile Ala Ser Ile Thr Leu Asp His
                        15          20          25

gaa ttt gta gtg cat gat att cgt gta att gat gga aac aat ggt ctt      629
Glu Phe Val Val His Asp Ile Arg Val Ile Asp Gly Asn Asn Gly Leu
                        30          35          40

ttc gtt gcg atg cca agt aag cgt aca cct gat gga gaa ttt cgt gat      677
Phe Val Ala Met Pro Ser Lys Arg Thr Pro Asp Gly Glu Phe Arg Asp
                        45          50          55

atc gct cat cca atc aac tca agc acc cgc gga aaa att cag gac gcg      725
Ile Ala His Pro Ile Asn Ser Ser Thr Arg Gly Lys Ile Gln Asp Ala
                        60          65          70          75

gtg tta aat gaa tat cat cgt ttg ggt gac gtt gag gaa ata gaa tat      773
Val Leu Asn Glu Tyr His Arg Leu Gly Asp Val Glu Glu Ile Glu Tyr
                        80          85          90

gaa gaa att gga gct tct taaaaaagaa gggcttatgg ataagccctt      821
Glu Glu Ile Gly Ala Ser
                        95

tttgttttga aaaaaaatga tcttatcata ataaaatgac aatatatggg ttgtgtctgc      881
gtataacagt agcaggaagg taaagcatgc gaactcggat aacaaagcgc atgcagaagg      941
aatcaatccg tctccctgat cagttaatcc taaatatgct ctaaakatcc aaaatatgct      1001
gtcttgattt cccgatttct cattttggct tgcttgaaat caactcatat ttaggatata      1061
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gttagcagct ggtcaaggaa caagaatgaa atcaaagcta tataaagttc ttcacacctg      1181
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<210> 139

<211> 97

10295.204.ST25.txt

<212> PRT
 <213> Bacillus licheniformis

<400> 139

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Asp Ile Arg Val Ile Asp Gly Asn Asn Gly Leu Phe Val Ala Met Pro
 35 40 45

Ser Lys Arg Thr Pro Asp Gly Glu Phe Arg Asp Ile Ala His Pro Ile
 50 55 60

Asn Ser Ser Thr Arg Gly Lys Ile Gln Asp Ala Val Leu Asn Glu Tyr
 65 70 75 80

His Arg Leu Gly Asp Val Glu Glu Ile Glu Tyr Glu Glu Ile Gly Ala
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Ser

<210> 140
 <211> 1694
 <212> DNA
 <213> Bacillus licheniformis

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 <222> (501)..(1451)

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 aaaagcggag atctggagct ttg ttt tca gct gtt gga cta tcg ctg caa att 533
 Leu Phe Ser Ala Val Gly Leu Ser Leu Gln Ile
 1 5 10
 gat gat gga gca gtt tca gaa tca gcc gag ctt ttc cgg aaa att aaa 581
 Asp Asp Gly Ala Val Ser Glu Ser Ala Glu Leu Phe Arg Lys Ile Lys
 15 20 25

10295.204.ST25.txt

agg cag aag gaa acg gtt aag agc gcg gat gac atc att cag tac tat	629
Arg Gln Lys Glu Thr Val Lys Ser Ala Asp Asp Ile Ile Gln Tyr Tyr	
30 35 40	
ttt ttc ttt ttt tca ggc atg tat gag ttt tat gag aaa aac tat ttt	677
Phe Phe Phe Phe Ser Gly Met Tyr Glu Phe Tyr Glu Lys Asn Tyr Phe	
45 50 55	
gag gcg atc agc tgt tac aag aaa gcg gaa gcg aag ctg cat aaa ctg	725
Glu Ala Ile Ser Cys Tyr Lys Lys Ala Glu Ala Lys Leu His Lys Leu	
60 65 70 75	
acc gat gaa att gaa aaa gcg gaa ttt tat tat aaa atc gcg acc gcc	773
Thr Asp Glu Ile Glu Lys Ala Glu Phe Tyr Tyr Lys Ile Ala Thr Ala	
80 85 90	
tac tac caa ata gac gat cat ttc aga tcg ttg aac tac tcc gaa aaa	821
Tyr Tyr Gln Ile Asp Asp His Phe Arg Ser Leu Asn Tyr Ser Glu Lys	
95 100 105	
gcg ctc tca ctt ttc agc aag cat aaa gaa tac ata gac aaa acg atc	869
Ala Leu Ser Leu Phe Ser Lys His Lys Glu Tyr Ile Asp Lys Thr Ile	
110 115 120	
gga tgc gaa atg ata ctc gga tcg gtg cag ttt gaa ttg ttc cgc atc	917
Gly Cys Glu Met Ile Leu Gly Ser Val Gln Phe Glu Leu Phe Arg Ile	
125 130 135	
aaa caa gct gag gag cac tac ggg cgg gcg ctt gat cag gcc gtt gcc	965
Lys Gln Ala Glu Glu His Tyr Gly Arg Ala Leu Asp Gln Ala Val Ala	
140 145 150 155	
ctt caa aac cgg cga atc atc ggg ctg atc tat cat aat atg gga ctg	1013
Leu Gln Asn Arg Arg Ile Ile Gly Leu Ile Tyr His Asn Met Gly Leu	
160 165 170	
aac tat gcc aaa tgc ggc atg ccg ctt ttg gcg gag gag cac ttt aga	1061
Asn Tyr Ala Lys Cys Gly Met Pro Leu Leu Ala Glu Glu His Phe Arg	
175 180 185	
aaa gcc ctt tca atc ggt gtc cat gag caa tcg gtt ttt ggc att aac	1109
Lys Ala Leu Ser Ile Gly Val His Glu Gln Ser Val Phe Gly Ile Asn	
190 195 200	
acc ctt ttc gag ctg tct cac ctc atg tac aaa aac ggt tct ccc gaa	1157
Thr Leu Phe Glu Leu Ser His Leu Met Tyr Lys Asn Gly Ser Pro Glu	
205 210 215	
gaa gcg aga cgt ctc tgc aaa gag gga ttt acc aga tcg gcc gaa tta	1205
Glu Ala Arg Arg Leu Cys Lys Glu Gly Phe Thr Arg Ser Ala Glu Leu	
220 225 230 235	
gga gag gat gaa tac gca gcg aag ttc agg ctg att ttc gcc ctg tat	1253
Gly Glu Asp Glu Tyr Ala Ala Lys Phe Arg Leu Ile Phe Ala Leu Tyr	
240 245 250	
gac gct ggc cat ccg ctc gat att gaa ttt tcg ctt gaa tat atg agt	1301
Asp Ala Gly His Pro Leu Asp Ile Glu Phe Ser Leu Glu Tyr Met Ser	
255 260 265	
gat aaa cgg cta tgg ccg cat gtt gct gaa ctg aca aaa gat att gcc	1349
Asp Lys Arg Leu Trp Pro His Val Ala Glu Leu Thr Lys Asp Ile Ala	
270 275 280	
gac tat tac atg aag tca ggc gac cat gaa aaa agc gcg ctt tac ctg	1397
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285 290 295	

10295.204.ST25.txt

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 Ile Ile

ggaagcttca cagctgattc tgcagcacag gacggatcgt ttcagccatt gggaaagtcg 1561

gtgtttcctg ccagcggacg atagagataa cttgccgaga tagaaatggc ctcccgtctt 1621

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gatttcgcgc tgc 1694

<210> 141

<211> 317

<212> PRT

<213> Bacillus licheniformis

<400> 141

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 20 25 30

Val Lys Ser Ala Asp Asp Ile Ile Gln Tyr Tyr Phe Phe Phe Ser
 35 40 45

Gly Met Tyr Glu Phe Tyr Glu Lys Asn Tyr Phe Glu Ala Ile Ser Cys
 50 55 60

Tyr Lys Lys Ala Glu Ala Lys Leu His Lys Leu Thr Asp Glu Ile Glu
 65 70 75 80

Lys Ala Glu Phe Tyr Tyr Lys Ile Ala Thr Ala Tyr Tyr Gln Ile Asp
 85 90 95

Asp His Phe Arg Ser Leu Asn Tyr Ser Glu Lys Ala Leu Ser Leu Phe
 100 105 110

Ser Lys His Lys Glu Tyr Ile Asp Lys Thr Ile Gly Cys Glu Met Ile
 115 120 125

Leu Gly Ser Val Gln Phe Glu Leu Phe Arg Ile Lys Gln Ala Glu Glu
 130 135 140

His Tyr Gly Arg Ala Leu Asp Gln Ala Val Ala Leu Gln Asn Arg Arg
 145 150 155 160

Ile Ile Gly Leu Ile Tyr His Asn Met Gly Leu Asn Tyr Ala Lys Cys
 165 170 175

10295.204.ST25.txt

Gly Met Pro Leu Leu Ala Glu Glu His Phe Arg Lys Ala Leu Ser Ile
 180 185 190

Gly Val His Glu Gln Ser Val Phe Gly Ile Asn Thr Leu Phe Glu Leu
 195 200 205

Ser His Leu Met Tyr Lys Asn Gly Ser Pro Glu Glu Ala Arg Arg Leu
 210 215 220

Cys Lys Glu Gly Phe Thr Arg Ser Ala Glu Leu Gly Glu Asp Glu Tyr
 225 230 235 240

Ala Ala Lys Phe Arg Leu Ile Phe Ala Leu Tyr Asp Ala Gly His Pro
 245 250 255

Leu Asp Ile Glu Phe Ser Leu Glu Tyr Met Ser Asp Lys Arg Leu Trp
 260 265 270

Pro His Val Ala Glu Leu Thr Lys Asp Ile Ala Asp Tyr Tyr Met Lys
 275 280 285

Ser Gly Asp His Glu Lys Ser Ala Leu Tyr Leu Glu Lys Ser Gln His
 290 295 300

Ala Lys Asn Gln Ile Tyr Lys Met Lys Glu Gly Ile Ile
 305 310 315

<210> 142
 <211> 1260
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1244)

<400> 142
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 cggccctcgg caccattgat cacacacatg ccggtgtggc ggaattggca gacgcgcacg 120
 actcaaaatc gtgttccttc gggagtgtcg gttcgacccc gaccaccggt atcactaaac 180
 atcgtattgc caaacgatga aagagcggtc ctacaaaagg agcgctcttt ttattttattc 240
 cttatcttgg aacgaagccg taagaatttt ttcttaagga ctgcgagctc cggaagctac 300
 gggaacatac cgtgagattt atcgaaatga gcttaatacg gtgcagaaac ttttacaaaa 360
 gcaaaaatat atctgatgat ttattatcta tttatagggc gaaaagtaaa ttattgatac 420
 aaacttcttt gcaaagattg gtaactttct gtaaaatgtt ctcatagcga tagaggcagt 480
 aaagtgtggg aggtttgaca atg aaa gca gca gcc tct gtg aac gta gcc aat 533
 Met Lys Ala Ala Ala Ser Val Asn Val Ala Asn
 1 5 10
 ctc atc aat cag tgg tat gtt cac ata aaa aag aga gat gtt tca aat 581

10295.204.ST25.txt

Leu Ile Asn Gln Trp Tyr Val His Ile Lys Lys Arg Asp Val Ser Asn
 15 20 25
 gcc gta gaa ctt agg gac aga ata aaa ggc ctt tta aac gta atg gaa 629
 Ala Val Glu Leu Arg Asp Arg Ile Lys Gly Leu Leu Asn Val Met Glu
 30 35 40
 gaa gat cag gat gtt ttg ctt tac ttt aat cta ctt gat tac agg ttc 677
 Glu Asp Gln Asp Val Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg Phe
 45 50 55
 aga gta tta atg gaa gac gtc gcg ggg gag ccg cag ctt ccg cct att 725
 Arg Val Leu Met Glu Asp Val Ala Gly Glu Pro Gln Leu Pro Pro Ile
 60 65 70 75
 gct gaa gat aag gcg aag aca gac ggt ttg tta cga tac tat tac ttt 773
 Ala Glu Asp Lys Ala Lys Thr Asp Gly Leu Leu Arg Tyr Tyr Tyr Phe
 80 85 90
 ctc ttt aaa gga atg tat gaa agt gcg agg agc aac tac tct aaa gcg 821
 Leu Phe Lys Gly Met Tyr Glu Ser Ala Arg Ser Asn Tyr Ser Lys Ala
 95 100 105
 ctt aat tgt ttt aga gtt gcc gag cgg cag ctc gat aat gtc gaa gat 869
 Leu Asn Cys Phe Arg Val Ala Glu Arg Gln Leu Asp Asn Val Glu Asp
 110 115 120
 gaa atc gaa aag gcc gag ttt cat tat aag ctt gga aat ctc tat tat 917
 Glu Ile Glu Lys Ala Glu Phe His Tyr Lys Leu Gly Asn Leu Tyr Tyr
 125 130 135
 ttt acg aaa aca act cta ctt tct ttt cat cat ctt tca atc gcg aag 965
 Phe Thr Lys Thr Thr Leu Leu Ser Phe His His Leu Ser Ile Ala Lys
 140 145 150 155
 agc att tat agg gct tat gaa gaa tat aag aca cag tcg ata aac tgt 1013
 Ser Ile Tyr Arg Ala Tyr Glu Glu Tyr Lys Thr Gln Ser Ile Asn Cys
 160 165 170
 acg gtg ctg ctc gca ctc aat tat ata gac gac gga cgt tta aca aga 1061
 Thr Val Leu Leu Ala Leu Asn Tyr Ile Asp Asp Gly Arg Leu Thr Arg
 175 180 185
 gct gaa aat atg ctt aag agt tgc gca gaa aga ctg atc aag atg ggc 1109
 Ala Glu Asn Met Leu Lys Ser Cys Ala Glu Arg Leu Ile Lys Met Gly
 190 195 200
 gat aat cat ctg ctg gcg gct gtc tac tat gat ctc ggc ttt tta aaa 1157
 Asp Asn His Leu Leu Ala Val Tyr Tyr Asp Leu Gly Phe Leu Lys
 205 210 215
 att caa gag gat aaa cat gaa gaa gca ctc gag tat ttc gac ctc tca 1205
 Ile Gln Glu Asp Lys His Glu Glu Ala Leu Glu Tyr Phe Asp Leu Ser
 220 225 230 235
 ttt aaa acg ggt gat atc gaa aaa aat gag ccg ggg act tagctcgata 1254
 Phe Lys Thr Gly Asp Ile Glu Lys Asn Glu Pro Gly Thr
 240 245
 gatgta 1260
 <210> 143
 <211> 248
 <212> PRT
 <213> Bacillus licheniformis
 <400> 143

10295.204.ST25.txt

Met Lys Ala Ala Ala Ser Val Asn Val Ala Asn Leu Ile Asn Gln Trp
 1 5 10 15
 Tyr Val His Ile Lys Lys Arg Asp Val Ser Asn Ala Val Glu Leu Arg
 20 25 30
 Asp Arg Ile Lys Gly Leu Leu Asn Val Met Glu Glu Asp Gln Asp Val
 35 40 45
 Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg Phe Arg Val Leu Met Glu
 50 55 60
 Asp Val Ala Gly Glu Pro Gln Leu Pro Pro Ile Ala Glu Asp Lys Ala
 65 70 75 80
 Lys Thr Asp Gly Leu Leu Arg Tyr Tyr Tyr Phe Leu Phe Lys Gly Met
 85 90 95
 Tyr Glu Ser Ala Arg Ser Asn Tyr Ser Lys Ala Leu Asn Cys Phe Arg
 100 105 110
 Val Ala Glu Arg Gln Leu Asp Asn Val Glu Asp Glu Ile Glu Lys Ala
 115 120 125
 Glu Phe His Tyr Lys Leu Gly Asn Leu Tyr Tyr Phe Thr Lys Thr Thr
 130 135 140
 Leu Leu Ser Phe His His Leu Ser Ile Ala Lys Ser Ile Tyr Arg Ala
 145 150 155 160
 Tyr Glu Glu Tyr Lys Thr Gln Ser Ile Asn Cys Thr Val Leu Leu Ala
 165 170 175
 Leu Asn Tyr Ile Asp Asp Gly Arg Leu Thr Arg Ala Glu Asn Met Leu
 180 185 190
 Lys Ser Cys Ala Glu Arg Leu Ile Lys Met Gly Asp Asn His Leu Leu
 195 200 205
 Ala Ala Val Tyr Tyr Asp Leu Gly Phe Leu Lys Ile Gln Glu Asp Lys
 210 215 220
 His Glu Glu Ala Leu Glu Tyr Phe Asp Leu Ser Phe Lys Thr Gly Asp
 225 230 235 240
 Ile Glu Lys Asn Glu Pro Gly Thr
 245

<210> 144
 <211> 2119
 <212> DNA

10295.204.ST25.txt

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1619)

<400> 144

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ttgatactaa	aggggggtgat	cagacttcga	tttgattgca	cccgaataaa	ctttatgttt	120
gtgtaccgca	gatataatct	attgcctatc	gattttctaa	aaggcgtaga	aatgtatctg	180
cggttttttc	tttagctttt	tatttcataa	aagaggtttg	aattttgctt	cctaacgatt	240
agttatgcca	aattacatat	caacaggaaa	atataatcct	tcatctgttc	tgctttcctt	300
cctatacttc	taaaattcac	ccaaacacgg	aaaacgaatc	atattgatta	ggccaaaaaa	360
cctctaactt	ataaagattt	ctgagaatgt	tggttgtaaa	aattattact	tttatgtaaa	420
atgatgacta	tgaataaaaa	gggaattgct	attttgggtt	tttagaaaaa	ttataatcct	480
gcgagaaagg	aagaggatat	gtg agc gtg ata cca tat gat ttg gtt gcg acg				533
		Val Ser Val Ile Pro Tyr Asp Leu Val Ala Thr				
		1 5 10				
aaa atg aat ttt tgg tat aca gcc tta.aaa aac aat tgg aca ggc aag						581
Lys Met Asn Phe Trp Tyr Thr Ala Leu Lys Asn Asn Trp Thr Gly Lys						
	15	20		25		
gct gag gat act aag aaa gaa gtt gaa cga gaa tta gaa caa atg gaa						629
Ala Glu Asp Thr Lys Lys Glu Val Glu Arg Glu Leu Glu Gln Met Glu						
	30	35		40		
caa aat cag gat gtg att gtc tat tac aac tta ctg ctc ttc cgg cat						677
Gln Asn Gln Asp Val Ile Val Tyr Tyr Asn Leu Leu Leu Phe Arg His						
	45	50		55		
aat ctt caa ctt gat tat atg tat tct aaa ccc ggt gta aat tta aat						725
Asn Leu Gln Leu Asp Tyr Met Tyr Ser Lys Pro Gly Val Asn Leu Asn						
	60	65		70		75
agt cgt ttt gat gag ttc aaa aag att cgc gat cag aat aat ctg gaa						773
Ser Arg Phe Asp Glu Phe Lys Lys Ile Arg Asp Gln Asn Asn Leu Glu						
	80			85		90
gga atg ttg gat tat tat tat cat ttt ttc gct gga atg tat cat ttc						821
Gly Met Leu Asp Tyr Tyr Tyr His Phe Phe Ala Gly Met Tyr His Phe						
	95			100		105
aga caa aaa gaa tta atc ctt gcg ctg aat ttt tat agg gat gcc gag						869
Arg Gln Lys Glu Leu Ile Leu Ala Leu Asn Phe Tyr Arg Asp Ala Glu						
	110			115		120
aaa aaa ctc gat tct ttt gat tgt gat gaa ctg gaa aag gct gaa ttt						917
Lys Lys Leu Asp Ser Phe Asp Cys Asp Glu Leu Glu Lys Ala Glu Phe						
	125			130		135
tat ttc aag gca tct gaa gtg tat tac cat atg aaa caa acc atc ttt						965
Tyr Phe Lys Ala Ser Glu Val Tyr Tyr His Met Lys Gln Thr Ile Phe						
	140			145		150
tcg atg aat tat gca agt cgt gcg tat aac tta ttc aaa aag tat gat						1013
Ser Met Asn Tyr Ala Ser Arg Ala Tyr Asn Leu Phe Lys Lys Tyr Asp						
	160			165		170

10295.204.ST25.txt

act tac ggt gag cgt cga gta caa agt cag ttt att att gca ggt aac	1061
Thr Tyr Gly Glu Arg Arg Val Gln Ser Gln Phe Ile Ile Ala Gly Asn	
175 180 185	
tgg cta gat cat atg tat ccc gaa aaa gct cta cat aat tta aat aaa	1109
Trp Leu Asp His Met Tyr Pro Glu Lys Ala Leu His Asn Leu Asn Lys	
190 195 200	
gag ctt aaa gag tca gag aca caa gga att ctt cat ctt atg ggt tca	1157
Glu Leu Lys Glu Ser Glu Thr Gln Gly Ile Leu His Leu Met Gly Ser	
205 210 215	
tca cat tta aat atc gga ata tgc tac aat aaa ttg gaa gat gtc gat	1205
Ser His Leu Asn Ile Gly Ile Cys Tyr Asn Lys Leu Glu Asp Val Asp	
220 225 230 235	
aaa gca acc tac aat ttt caa aga gct ctg aac ctt tat aaa gag gag	1253
Lys Ala Thr Tyr Asn Phe Gln Arg Ala Leu Asn Leu Tyr Lys Glu Glu	
240 245 250	
aag cat agt ttt ttg cca aaa aca tta ttc aac ctc gca cat gtc agg	1301
Lys His Ser Phe Leu Pro Lys Thr Leu Phe Asn Leu Ala His Val Arg	
255 260 265	
gca aag caa ggg aag ttg tca ata act gat gac cta tac tat gaa ggc	1349
Ala Lys Gln Gly Lys Leu Ser Ile Thr Asp Asp Leu Tyr Tyr Glu Gly	
270 275 280	
aaa gag ttg gct gaa aag aac aag aat tta gat atg ctt gca aag ttt	1397
Lys Glu Leu Ala Glu Lys Asn Lys Asn Leu Asp Met Leu Ala Lys Phe	
285 290 295	
gat tta ata aaa ggg ctt tat ctt tca ttt gat ctg gat atg gtt cgc	1445
Asp Leu Ile Lys Gly Leu Tyr Leu Ser Phe Asp Leu Asp Met Val Arg	
300 305 310 315	
gaa tcg ttc aag ttt ttc gaa agt aaa ggc aag tat gca gac atg gag	1493
Glu Ser Phe Lys Phe Phe Glu Ser Lys Gly Lys Tyr Ala Asp Met Glu	
320 325 330	
gaa tac ggt ctt ata gcg gct gaa cta tta gag aaa aaa gaa aaa att	1541
Glu Tyr Gly Leu Ile Ala Ala Glu Leu Leu Glu Lys Lys Glu Lys Ile	
335 340 345	
cga gat gca gtg gaa ttc tac cgg ata aca gtt aat gcg aga aga caa	1589
Arg Asp Ala Val Glu Phe Tyr Arg Ile Thr Val Asn Ala Arg Arg Gln	
350 355 360	
att caa agg agt gct ttt cta cat gta aac taaatcggtc taggggtagt	1639
Ile Gln Arg Ser Ala Phe Leu His Val Asn	
365 370	
taaagcagca ggattttctta ctataaaaaa gaatttcccc cagcattatt aaaacctcaa	1699
attttgatta cttgattatt attttaagta atcgagaaaa gaaagggtcgg tctatggcaa	1759
gctattttaaa atccagaatc gtatcttatc tgtttattct tttggaagtg gggaccggat	1819
tcgcaatttg cgagggtgtca atggaaaatc cgaattactc ctcagcttgc gcggtcttta	1879
tcatagggttt tacgattggg gaatgcttca tgattagaaa atggtaaatt ttgatcatga	1939
cgggatactc tttacctctt tctataaaag tgggacagac agttgaaaag ccggtaaatt	1999
catagccttg tatttcaaca gtaacttctt ctatatgcgg gtttcatttt ttcattcttg	2059
cttaatacat taaatcacct cttttataca gtatttgtcc attaaagaag aacaggatct	2119

10295.204.ST25.txt

<210> 145
 <211> 373
 <212> PRT
 <213> Bacillus licheniformis

<400> 145

Val Ser Val Ile Pro Tyr Asp Leu Val Ala Thr Lys Met Asn Phe Trp
 1 5 10 15
 Tyr Thr Ala Leu Lys Asn Asn Trp Thr Gly Lys Ala Glu Asp Thr Lys
 20 25 30
 Lys Glu Val Glu Arg Glu Leu Glu Gln Met Glu Gln Asn Gln Asp Val
 35 40 45
 Ile Val Tyr Tyr Asn Leu Leu Leu Phe Arg His Asn Leu Gln Leu Asp
 50 55 60
 Tyr Met Tyr Ser Lys Pro Gly Val Asn Leu Asn Ser Arg Phe Asp Glu
 65 70 75 80
 Phe Lys Lys Ile Arg Asp Gln Asn Asn Leu Glu Gly Met Leu Asp Tyr
 85 90 95
 Tyr Tyr His Phe Phe Ala Gly Met Tyr His Phe Arg Gln Lys Glu Leu
 100 105 110
 Ile Leu Ala Leu Asn Phe Tyr Arg Asp Ala Glu Lys Lys Leu Asp Ser
 115 120 125
 Phe Asp Cys Asp Glu Leu Glu Lys Ala Glu Phe Tyr Phe Lys Ala Ser
 130 135 140
 Glu Val Tyr Tyr His Met Lys Gln Thr Ile Phe Ser Met Asn Tyr Ala
 145 150 155 160
 Ser Arg Ala Tyr Asn Leu Phe Lys Lys Tyr Asp Thr Tyr Gly Glu Arg
 165 170 175
 Arg Val Gln Ser Gln Phe Ile Ile Ala Gly Asn Trp Leu Asp His Met
 180 185 190
 Tyr Pro Glu Lys Ala Leu His Asn Leu Asn Lys Glu Leu Lys Glu Ser
 195 200 205
 Glu Thr Gln Gly Ile Leu His Leu Met Gly Ser Ser His Leu Asn Ile
 210 215 220
 Gly Ile Cys Tyr Asn Lys Leu Glu Asp Val Asp Lys Ala Thr Tyr Asn
 225 230 235 240

10295.204.ST25.txt

Phe Gln Arg Ala Leu Asn Leu Tyr Lys Glu Glu Lys His Ser Phe Leu
245 250 255

Pro Lys Thr Leu Phe Asn Leu Ala His Val Arg Ala Lys Gln Gly Lys
260 265 270

Leu Ser Ile Thr Asp Asp Leu Tyr Tyr Glu Gly Lys Glu Leu Ala Glu
275 280 285

Lys Asn Lys Asn Leu Asp Met Leu Ala Lys Phe Asp Leu Ile Lys Gly
290 295 300

Leu Tyr Leu Ser Phe Asp Leu Asp Met Val Arg Glu Ser Phe Lys Phe
305 310 315 320

Phe Glu Ser Lys Gly Lys Tyr Ala Asp Met Glu Glu Tyr Gly Leu Ile
325 330 335

Ala Ala Glu Leu Leu Glu Lys Lys Glu Lys Ile Arg Asp Ala Val Glu
340 345 350

Phe Tyr Arg Ile Thr Val Asn Ala Arg Arg Gln Ile Gln Arg Ser Ala
355 360 365

Phe Leu His Val Asn
370

<210> 146
<211> 1405
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(905)

<400> 146
tgtagggaaa gtgagttcat ggctcttatt agtgattgtc agctttctaa tcgtagccac 60
gttaaaacag gtgaaggga aagattccac tagagtggat gctgggtcaat tttataact 120
ctttatttta aaagggtttc gaggagctgt ggaagctgtt gcaggcatca ataaaagatc 180
aatattttct ttaagttgat cattcacaaa tcgaattact tctttattag gccaagtttc 240
atttcatgg atgcacaggg tttatccgca aattccttca aatagtaaac cttcaagat 300
cgcggtggac gaaatttccc ttcgagaata ctgcagggtc ggcttgaaaa agagcatata 360
gagattcagg cgtcttagca ggcgtctttt tgttgctgat tttattgcgg cataccgaaa 420
atttttcac ttttcaacct attatcacc gaattatagt aatatattta caaaaatgaa 480
ataaaaaggt ataggcggaa gtg aaa cag tta ata ccc tcg tca aaa gtc gga 533
Val Lys Gln Leu Ile Pro Ser Ser Lys Val Gly
1 5 10
gtg aaa atc cac gaa tgg tat aaa atg ata aga gag ttt agc gta ccg 581

10295.204.ST25.txt

val Lys Ile His Glu Trp Tyr Lys Met Ile Arg Glu Phe Ser Val Pro
 15 20 25
 gat gca gag gct tta aaa gaa gaa gta gag aag gaa att aat caa atg 629
 Asp Ala Glu Ala Leu Lys Glu Glu Val Glu Lys Glu Ile Asn Gln Met
 30 35 40
 gaa gaa gat cag gac tta ctc ctt tac tat cag ttg atg tgt ttt aga 677
 Glu Glu Asp Gln Asp Leu Leu Tyr Tyr Gln Leu Met Cys Phe Arg
 45 50 55
 cat caa tta atg tta gaa tat tta gaa cct act aac aaa aga aaa caa 725
 His Gln Leu Met Leu Glu Tyr Leu Glu Pro Thr Asn Lys Arg Lys Gln
 60 65 70 75
 gga caa tca ata aac aaa ttg ttg gcc caa atc gag gag cct cga aga 773
 Gly Gln Ser Ile Asn Lys Leu Leu Ala Gln Ile Glu Glu Pro Arg Arg
 80 85 90
 gat tta aat ggc ctc ctt agt tac tac tca ttt ttc ttt agg ggc atg 821
 Asp Leu Asn Gly Leu Leu Ser Tyr Tyr Ser Phe Phe Phe Arg Gly Met
 95 100 105
 tat gaa ttt gag aaa aaa cag tac atc aaa gca ata gag ttt tat cga 869
 Tyr Glu Phe Glu Lys Lys Gln Tyr Ile Lys Ala Ile Glu Phe Tyr Arg
 110 115 120
 aac gca gaa aaa cag ttg gct ctc att acg atg tta tagaacaagc 915
 Asn Ala Glu Lys Gln Leu Ala Leu Ile Thr Met Leu
 125 130 135
 cgagtttcac tttaaaatgg ctgaagcata ctacatcatg aaacagacac atgtatcata 975
 tattaagggc ctttaaaata tacaataatc atgaactcta cacagtccgt aaaatccaat 1035
 gttttattgt tatcgcgggg aactatgacg atttaatgcg ccatgacaaa gccttacccc 1095
 acctggaaaa tgcacttgaa ttagcgatag agatcgacaa taaaaggctc attagttctg 1155
 cctatttttaa tatagccgac tgtcatgaat gtatgggaga cattgatgca gcagttgaat 1215
 atgctgaaaa agccgtagag attaattctaa aagaagaata taacaaccta ccacaatcat 1275
 tatattactc tactcaactt ctttttaagc agaaaaacta cgagcgcgca atcgagatat 1335
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 gaatatcttg 1405

<210> 147
 <211> 135
 <212> PRT
 <213> Bacillus licheniformis

<400> 147

val Lys Gln Leu Ile Pro Ser Ser Lys Val Gly Val Lys Ile His Glu
 1 5 10 15

Trp Tyr Lys Met Ile Arg Glu Phe Ser Val Pro Asp Ala Glu Ala Leu
 20 25 30

Lys Glu Glu Val Glu Lys Glu Ile Asn Gln Met Glu Glu Asp Gln Asp
 35 40 45

10295.204.ST25.txt

Leu Leu Leu Tyr Tyr Gln Leu Met Cys Phe Arg His Gln Leu Met Leu
 50 55 60

Glu Tyr Leu Glu Pro Thr Asn Lys Arg Lys Gln Gly Gln Ser Ile Asn
 65 70 75 80

Lys Leu Leu Ala Gln Ile Glu Glu Pro Arg Arg Asp Leu Asn Gly Leu
 85 90 95

Leu Ser Tyr Tyr Ser Phe Phe Phe Arg Gly Met Tyr Glu Phe Glu Lys
 100 105 110

Lys Gln Tyr Ile Lys Ala Ile Glu Phe Tyr Arg Asn Ala Glu Lys Gln
 115 120 125

Leu Ala Leu Ile Thr Met Leu
 130 135

<210> 148
 <211> 2104
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1604)

<400> 148
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 gacgatatcg gctttttgat cgcgaacca gcgtcccca accattccgc tgtgaatgcg 120
 gtaatcgatg gtatggatcat ttttaatgta gatttcatat tcccatccgt tttcatacgt 180
 atagatcata tggcttccta caaactcttt tacatcttga ttcatatgaa ccgctccttt 240
 atttgtttat tgtaatcgaa acatgttgat atttcatat ataattataa aatgccgtca 300
 aaaaagatgt caaacgaaaa tacttctga gagatttgca caaataaaga agattgttac 360
 gattaatgtc agaattttga gttatcttag gaaattatgc caatatttag aaaagtgatt 420
 gtcaaaaaat aagcgattct gtaaaatgaa aaacaacca taaaaaggaa atgacatggg 480
 aagaaaggaa ggataaacga ttg aag aca aaa att gcg tat gag gaa gtt gcg 533
 Leu Lys Thr Lys Ile Ala Tyr Glu Glu Val Ala 10
 1
 gga atg ctt aat caa tgg tat gtc atg atc aag cgt cac gaa gta tca 581
 Gly Met Leu Asn Gln Trp Tyr Val Met Ile Lys Arg His Glu Val Ser 25
 15 20
 caa gcg gtc tcg att aaa tgc gac att gag cac cag ctg ccg aat atg 629
 Gln Ala Val Ser Ile Lys Cys Asp Ile Glu His Gln Leu Pro Asn Met 40
 30 35
 gaa gaa aat caa gat ctg ctt ctt tat ttt aat ctt tta gac tat cg 677
 Glu Glu Asn Gln Asp Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg 55
 45 50

10295.204.ST25.txt

cac aag ctg ctg aca gaa gag ttt gcc gct tcc aac aaa ctg ttc gag His Lys Leu Leu Thr Glu Glu Phe Ala Ala Ser Asn Lys Leu Phe Glu 60 65 70 75	725
gat att cag gag caa aaa gcc gat atg caa agc aca gat gac atg att Asp Ile Gln Glu Gln Lys Ala Asp Met Gln Ser Thr Asp Asp Met Ile 80 85 90	773
gaa tat tat tat ttc ttt ttc gct ggc atg tac gaa ttt cat aag aag Glu Tyr Tyr Tyr Phe Phe Phe Ala Gly Met Tyr Glu Phe His Lys Lys 95 100 105	821
gat tat aca aat gca atc aat tat tat aaa tta gcc gag gaa aag ctc Asp Tyr Thr Asn Ala Ile Asn Tyr Tyr Lys Leu Ala Glu Glu Lys Leu 110 115 120	869
agg aca atc ccc gat caa atc gaa atc gcc gaa ttc cat tac aaa ctg Arg Thr Ile Pro Asp Gln Ile Glu Ile Ala Glu Phe His Tyr Lys Leu 125 130 135	917
gct atc gcc tac tat caa atc aaa caa aat ttc ctt tcc tta aac cat Ala Ile Ala Tyr Tyr Gln Ile Lys Gln Asn Phe Leu Ser Leu Asn His 140 145 150 155	965
gcg aaa aca gct cta aaa acc ttc aaa gca cat gat gat tac att caa Ala Lys Thr Ala Leu Lys Thr Phe Lys Ala His Asp Asp Tyr Ile Gln 160 165 170	1013
aaa gcg atc agc aac gat atg ctg atc ggg gca aat aaa ctc gat tta Lys Ala Ile Ser Asn Asp Met Leu Ile Gly Ala Asn Lys Leu Asp Leu 175 180 185	1061
ttt cgt ttt gat gaa gcc gaa cag cat tac aag caa gcc ctt aaa gac Phe Arg Phe Asp Glu Ala Glu Gln His Tyr Lys Gln Ala Leu Lys Asp 190 195 200	1109
gcg gca ctg atc aaa cat cat gtc ctc ctc ggc atg gct cac cac aac Ala Ala Leu Ile Lys His His Val Leu Leu Gly Met Ala His His Asn 205 210 215	1157
tta ggg ttg agc tat gtc aat cgc aac ctc ctc aca ttg gct gaa cat Leu Gly Leu Ser Tyr Val Asn Arg Asn Leu Leu Thr Leu Ala Glu His 220 225 230 235	1205
cat ttc aaa gaa gcg ctg ctt atc aaa gag cat gaa gaa tcg gtt tac His Phe Lys Glu Ala Leu Leu Ile Lys Glu His Glu Glu Ser Val Tyr 240 245 250	1253
ggc atc cat tcc atg ttt gaa ctg aca cat gtg ctg tac aaa tca aat Gly Ile His Ser Met Phe Glu Leu Thr His Val Leu Tyr Lys Ser Asn 255 260 265	1301
gtt gtc aaa gaa gca cgc aaa ttg tat gaa aaa gga ttt ttc cgt gcg Val Val Lys Glu Ala Arg Lys Leu Tyr Glu Lys Gly Phe Phe Arg Ala 270 275 280	1349
gaa aaa gca gga gaa agg gaa tat ttg tcg aaa ttt aaa ctt att cat Glu Lys Ala Gly Glu Arg Glu Tyr Leu Ser Lys Phe Lys Leu Ile His 285 290 295	1397
gct ctg tat gat gaa cag gat cca ctt acg gtt gaa cat gct tta gaa Ala Leu Tyr Asp Glu Gln Asp Pro Leu Thr Val Glu His Ala Leu Glu 300 305 310 315	1445
tat ctt aaa acg atc aat ctc tgg acg gat gta gcg gaa tta aca ttt Tyr Leu Lys Thr Ile Asn Leu Trp Thr Asp Val Ala Glu Leu Thr Phe 320 325 330	1493

10295.204.ST25.txt

gat atc gca ctt tac tat aaa gaa aat gga gat gca gac aaa gct gcc 1541
 Asp Ile Ala Leu Tyr Tyr Lys Glu Asn Gly Asp Ala Asp Lys Ala Ala
 335 340 345
 gaa tat ttt gaa gaa tct cat cat gca aga gac caa att ctt aaa aga 1589
 Glu Tyr Phe Glu Glu Ser His His Ala Arg Asp Gln Ile Leu Lys Arg
 350 355 360
 acg gag gag tta aag tgaaaaagat gattgccgtt gcgttgactg ccgtctttgc 1644
 Thr Glu Glu Leu Lys
 365
 aagccttgct gttttaagtt tttcgtctca gccgaaggga gatgccgagt ttgccggccg 1704
 agccattttt cttgacgata agccggctca gctgatggcg ggcagagcga tctttctcga 1764
 cagctttgac ggaaattcgc cagccgcctg acaaaacacc gcataaccct gcttgtcacc 1824
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 ctcaccggct tttggctgaa tcctattgaa aaatctgccc gatttatagt gcttgtcatt 2004
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<210> 149
 <211> 368
 <212> PRT
 <213> Bacillus licheniformis

<400> 149

Leu Lys Thr Lys Ile Ala Tyr Glu Glu Val Ala Gly Met Leu Asn Gln
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Trp Tyr Val Met Ile Lys Arg His Glu Val Ser Gln Ala Val Ser Ile
 20 25 30

Lys Cys Asp Ile Glu His Gln Leu Pro Asn Met Glu Glu Asn Gln Asp
 35 40 45

Leu Leu Leu Tyr Phe Asn Leu Leu Asp Tyr Arg His Lys Leu Leu Thr
 50 55 60

Glu Glu Phe Ala Ala Ser Asn Lys Leu Phe Glu Asp Ile Gln Glu Gln
 65 70 75 80

Lys Ala Asp Met Gln Ser Thr Asp Asp Met Ile Glu Tyr Tyr Tyr Phe
 85 90 95

Phe Phe Ala Gly Met Tyr Glu Phe His Lys Lys Asp Tyr Thr Asn Ala
 100 105 110

Ile Asn Tyr Tyr Lys Leu Ala Glu Glu Lys Leu Arg Thr Ile Pro Asp
 115 120 125

10295.204.ST25.txt

Gln Ile Glu Ile Ala Glu Phe His Tyr Lys Leu Ala Ile Ala Tyr Tyr
 130 135 140

Gln Ile Lys Gln Asn Phe Leu Ser Leu Asn His Ala Lys Thr Ala Leu
 145 150 155 160

Lys Thr Phe Lys Ala His Asp Asp Tyr Ile Gln Lys Ala Ile Ser Asn
 165 170 175

Asp Met Leu Ile Gly Ala Asn Lys Leu Asp Leu Phe Arg Phe Asp Glu
 180 185 190

Ala Glu Gln His Tyr Lys Gln Ala Leu Lys Asp Ala Ala Leu Ile Lys
 195 200 205

His His Val Leu Leu Gly Met Ala His His Asn Leu Gly Leu Ser Tyr
 210 215 220

Val Asn Arg Asn Leu Leu Thr Leu Ala Glu His His Phe Lys Glu Ala
 225 230 235 240

Leu Leu Ile Lys Glu His Glu Glu Ser Val Tyr Gly Ile His Ser Met
 245 250 255

Phe Glu Leu Thr His Val Leu Tyr Lys Ser Asn Val Val Lys Glu Ala
 260 265 270

Arg Lys Leu Tyr Glu Lys Gly Phe Phe Arg Ala Glu Lys Ala Gly Glu
 275 280 285

Arg Glu Tyr Leu Ser Lys Phe Lys Leu Ile His Ala Leu Tyr Asp Glu
 290 295 300

Gln Asp Pro Leu Thr Val Glu His Ala Leu Glu Tyr Leu Lys Thr Ile
 305 310 315 320

Asn Leu Trp Thr Asp Val Ala Glu Leu Thr Phe Asp Ile Ala Leu Tyr
 325 330 335

Tyr Lys Glu Asn Gly Asp Ala Asp Lys Ala Ala Glu Tyr Phe Glu Glu
 340 345 350

Ser His His Ala Arg Asp Gln Ile Leu Lys Arg Thr Glu Glu Leu Lys
 355 360 365

<210> 150
 <211> 1381
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS

10295.204.ST25.txt

<222> (501)..(881)

<400> 150

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aagtcgggagt gaaaatccac gaatggtata aaatgataag agagtttagc gtaccggatg      120
cagaggccttt aaaagaagaa gtagagaagg aaattaatca aatggaagaa gatcaggact      180
tactccttta ctatcagttg atgtgtttta gacatcaatt aatgttagaa tatttagaac      240
ctactaacia aagaaaacia ggacaatcaa taaacaaatt gttggcccaa atcgaggagc      300
ctcgaagaga tttaaatggc ctccttagtt actactcatt tttctttagg ggcattgtatg      360
aatttgagaa aaaacagtac atcaaagcaa tagagtttta tcgaaacgca gaaaaacagt      420
tggctctcat tacgatgtta tagaacaagc cgagtttcac tttaaaatgg ctgaagcata      480
ctacatcatg aaacagacac atg tat cat ata tta agg gcc ttt aaa ata tac      533
                      Met Tyr His Ile Leu Arg Ala Phe Lys Ile Tyr
                      1       5       10

aat aat cat gaa ctc tac aca gtc cgt aaa atc caa tgt tta ttt gtt      581
Asn Asn His Glu Leu Tyr Thr Val Arg Lys Ile Gln Cys Leu Phe Val
                      15       20       25

atc gcg ggt aac tat gac gat tta atg cgc cat gac aaa gcc tta ccc      629
Ile Ala Gly Asn Tyr Asp Asp Leu Met Arg His Asp Lys Ala Leu Pro
                      30       35       40

cac ctg gaa aat gca ctt gaa tta gcg ata gag atc gac aat aaa agg      677
His Leu Glu Asn Ala Leu Glu Leu Ala Ile Glu Ile Asp Asn Lys Arg
                      45       50       55

ctc att agt tct gcc tat ttt aat ata gcc gac tgt cat gaa tgt atg      725
Leu Ile Ser Ser Ala Tyr Phe Asn Ile Ala Asp Cys His Glu Cys Met
60       65       70       75

gga gac att gat gca gca gtt gaa tat gct gaa aaa gcc gta gag att      773
Gly Asp Ile Asp Ala Ala Val Glu Tyr Ala Glu Lys Ala Val Glu Ile
                      80       85       90

aat cta aaa gaa gaa tat aac aac cta cca caa tca tta tat tac tct      821
Asn Leu Lys Glu Glu Tyr Asn Asn Leu Pro Gln Ser Leu Tyr Tyr Ser
                      95      100      105

act caa ctt ctt ttt aag cag aaa aac tac gag cgc gca atc gag ata      869
Thr Gln Leu Leu Phe Lys Gln Lys Asn Tyr Glu Arg Ala Ile Glu Ile
110      115      120

ttt ctt att ggt tagacaaaca gctcgaaaat tcaacgatac cctattcact      921
Phe Leu Ile Gly
125

tctctatttg aatatcttga ggcggttatat atctattctg tgaataaaga agagatttta      981
gaggtattta aatacttgga ggagaataaa atatttgcac acatagaaga gctttcgtt      1041
gaagtctcta accaatacct tgaaagaaaa gaccatagaa actcaatcga gttccttcaa      1101
aaaatgatgt atgggcaaac aaaaattaaa aaaggggagt gtctctatga gtattaaaaa      1161
gctcgttatt cccatttttag ccgccgcgtt attaacgatg ggtatttagcg ttgtttcagc      1221
aaccgaccag tctgacggcg tatatcaaat cgctaccgct aagcaaacgt aagaaacgcc      1281
ccaaatgtgg ggcgcttttt atttctacgg tttcttaacg ttaaacatcg tgattaactt      1341

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10295.204.ST25.txt

cttatcagct gtcggttaaga ttaacgtata ccattccgac

1381

<210> 151
 <211> 127
 <212> PRT
 <213> Bacillus licheniformis

<400> 151

Met Tyr His Ile Leu Arg Ala Phe Lys Ile Tyr Asn Asn His Glu Leu
 1 5 10 15

Tyr Thr Val Arg Lys Ile Gln Cys Leu Phe Val Ile Ala Gly Asn Tyr
 20 25 30

Asp Asp Leu Met Arg His Asp Lys Ala Leu Pro His Leu Glu Asn Ala
 35 40 45

Leu Glu Leu Ala Ile Glu Ile Asp Asn Lys Arg Leu Ile Ser Ser Ala
 50 55 60

Tyr Phe Asn Ile Ala Asp Cys His Glu Cys Met Gly Asp Ile Asp Ala
 65 70 75 80

Ala Val Glu Tyr Ala Glu Lys Ala Val Glu Ile Asn Leu Lys Glu Glu
 85 90 95

Tyr Asn Asn Leu Pro Gln Ser Leu Tyr Tyr Ser Thr Gln Leu Leu Phe
 100 105 110

Lys Gln Lys Asn Tyr Glu Arg Ala Ile Glu Ile Phe Leu Ile Gly
 115 120 125

<210> 152
 <211> 1735
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1235)

<400> 152
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 tcgcagacgc cgtattcagc ggggactccg gccgttttgc gcgcatttat cttgaaaagc 180
 ttctgcacgc tccgctggca gcgatgattg agacaaaaa gatctatcag gcgttgaatg 240
 gaggcaggct gcagaaaacg cttgaactcg agaaaacggc ccagatgaaa atgaggctga 300
 caagcgacca tcaggaaggg atccgcgcgc ttttagaaaa gcgccagccg caatttaacc 360
 gtcagcaagt ataacaagag cgggtccggc ggaaattgac cttgggaaat gatgtgcaga 420

10295.204.ST25.txt

aacaattgta aaaaaattta agtttccata aaatgattca taagatacag atctgtacga 480
agtccttgga ggcggcgaaa ttg aaa cag aag att cca tct gaa tac gtt gct 533
Leu Lys Gln Lys Ile Pro Ser Glu Tyr Val Ala
1 5 10
aga aag ctg aat gat tgg tac aac gcc att cgg aaa aat cag atc gcc 581
Arg Lys Leu Asn Asp Trp Tyr Asn Ala Ile Arg Lys Asn Gln Ile Ala
15 20 25
gcc agt gaa tca ttg aaa gcg gaa att tta aat gat ttt caa gac atg 629
Ala Ser Glu Ser Leu Lys Ala Glu Ile Leu Asn Asp Phe Gln Asp Met
30 35 40
gaa gaa aat cgg gac gtc ctg ctc tac tat tgc ctg ctt gaa ttc agg 677
Glu Glu Asn Arg Asp Val Leu Leu Tyr Tyr Ser Leu Leu Glu Phe Arg
45 50 55
cat aaa ctg atg ctc agc tat ttg aaa ccg aaa gag act gaa aat att 725
His Lys Leu Met Leu Ser Tyr Leu Lys Pro Lys Glu Thr Glu Asn Ile
60 65 70 75
gaa aaa aac ctc cgc gac tta gaa gaa aaa gaa gac caa atg acg ggt 773
Glu Lys Asn Leu Arg Asp Leu Glu Glu Lys Glu Asp Gln Met Thr Gly
80 85 90
tta tta aac tat tat tac tgg ttt ttt aaa ggg atg tat gag ttc aaa 821
Leu Leu Asn Tyr Tyr Tyr Trp Phe Phe Lys Gly Met Tyr Glu Phe Lys
95 100 105
caa aag cgg ttc gtc aaa gca atc ggc tgc tat aaa acg gct gaa caa 869
Gln Lys Arg Phe Val Lys Ala Ile Gly Cys Tyr Lys Thr Ala Glu Gln
110 115 120
aaa gtc agc gca ctg gaa gac gag gtt gaa aaa gcg gaa ttt tat tat 917
Lys Val Ser Ala Leu Glu Asp Glu Val Glu Lys Ala Glu Phe Tyr Tyr
125 130 135
aag ctt gcg gaa atc tac tat tat atc aac cag aga tac ctg tgc atc 965
Lys Leu Ala Glu Ile Tyr Tyr Tyr Ile Asn Gln Arg Tyr Leu Ser Ile
140 145 150 155
aac tat gcg acg cta gct tcc gac att ttt aac cgg tat gaa acg cta 1013
Asn Tyr Ala Thr Leu Ala Ser Asp Ile Phe Asn Arg Tyr Glu Thr Leu
160 165 170
aaa gaa aaa aag att ttc tgc gat ttt atc att gcc ggt aat tgg gtt 1061
Lys Glu Lys Lys Ile Phe Cys Asp Phe Ile Ile Ala Gly Asn Trp Val
175 180 185
gaa tgc atg aca tac gga ccc gcg ctg aaa agc ctg gcc aat gcg ctt 1109
Glu Ser Met Thr Tyr Gly Pro Ala Leu Lys Ser Leu Ala Asn Ala Leu
190 195 200
gaa gac gcc agg aaa atc aaa aac agc cat ttg acg gca gcc gct cat 1157
Glu Asp Ala Arg Lys Ile Lys Asn Ser His Leu Thr Ala Ala Ala His
205 210 215
ttt aat ttg gga aat tgc tat ttc cac caa gaa tgc tac cgg gaa gcc 1205
Phe Asn Leu Gly Asn Cys Tyr Phe His Gln Glu Ser Tyr Arg Glu Ala
220 225 230 235
tca gat cat atg gag cgc cct ttc cat ttt tgaacaggaa agttcatcat 1255
Ser Asp His Met Glu Arg Pro Phe His Phe
240 245
atattcccaa agtgctgtac aacttgatgt acgtccgtct caagcagggg aaccatgccg 1315

10295.204.ST25.txt

gagctgccgc ctgttatgaa aaagggcatcc gaagcgcggc atcgctcggg gatgaagaac 1375
 acgcggcaaa gcttaacatt ctgtgcgggc tgtatttaga cggaggggat cagaaagccg 1435
 tggaaaacgg atttgattat ttggagtcaa atcatttata tgctgctgtt gaagagctgg 1495
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 aaactgttgt tcgtcgcggg gtcgctgggt gttgtgttaa cgtcttcaag ctttttggca 1675
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<210> 153
 <211> 245
 <212> PRT
 <213> Bacillus licheniformis

<400> 153

Leu Lys Gln Lys Ile Pro Ser Glu Tyr Val Ala Arg Lys Leu Asn Asp
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Trp Tyr Asn Ala Ile Arg Lys Asn Gln Ile Ala Ala Ser Glu Ser Leu
20 25 30

Lys Ala Glu Ile Leu Asn Asp Phe Gln Asp Met Glu Glu Asn Arg Asp
35 40 45

Val Leu Leu Tyr Tyr Ser Leu Leu Glu Phe Arg His Lys Leu Met Leu
50 55 60

Ser Tyr Leu Lys Pro Lys Glu Thr Glu Asn Ile Glu Lys Asn Leu Arg
65 70 75 80

Asp Leu Glu Glu Lys Glu Asp Gln Met Thr Gly Leu Leu Asn Tyr Tyr
85 90 95

Tyr Trp Phe Phe Lys Gly Met Tyr Glu Phe Lys Gln Lys Arg Phe Val
100 105 110

Lys Ala Ile Gly Cys Tyr Lys Thr Ala Glu Gln Lys Val Ser Ala Leu
115 120 125

Glu Asp Glu Val Glu Lys Ala Glu Phe Tyr Tyr Lys Leu Ala Glu Ile
130 135 140

Tyr Tyr Tyr Ile Asn Gln Arg Tyr Leu Ser Ile Asn Tyr Ala Thr Leu
145 150 155 160

Ala Ser Asp Ile Phe Asn Arg Tyr Glu Thr Leu Lys Glu Lys Lys Ile
165 170 175

Phe Cys Asp Phe Ile Ile Ala Gly Asn Trp Val Glu Ser Met Thr Tyr
180 185 190

10295.204.ST25.txt

Gly Pro Ala Leu Lys Ser Leu Ala Asn Ala Leu Glu Asp Ala Arg Lys
 195 200 205

Ile Lys Asn Ser His Leu Thr Ala Ala Ala His Phe Asn Leu Gly Asn
 210 215 220

Cys Tyr Phe His Gln Glu Ser Tyr Arg Glu Ala Ser Asp His Met Glu
 225 230 235 240

Arg Pro Phe His Phe
 245

<210> 154
 <211> 2116
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1616)

<400> 154
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 gttccagcgt ttgatctatt gcattgtgca gcgctgaac atcaagagtc ttcattggcat 180
 tctcctctaa tccttttcat tacaatcagt atatagtta ccactttata gaaagtactt 240
 ggtgaatata tcctgttcaa ccatgaaaat gaatcattgg gcttaggtca ttatttctat 300
 tgattcattt cgattaccgt aaacaagttt gttgtagcat tcttaggct ctgtgactaa 360
 accaaaaagc catttgtttt aaattgggtct ttcggtatca cgaaaatttc gttttttggg 420
 ctgatagaag ttttgcaatt atgaattgta tgtaaatctt taacataaaa aggatgtag 480
 ctggaaggga atgatggcag ttg gag act atc ccg tct tca gaa gtt gga atc 533
 Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile
 1 5 10
 aaa ata aac cgc tgg tac aac gaa att caa aaa tta aac gta ata gaa 581
 Lys Ile Asn Arg Trp Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu
 15 20 25
 gca gaa cga tta aag gcg gaa gtt cac tta gct ata gaa aga atg gaa 629
 Ala Glu Arg Leu Lys Ala Glu Val His Leu Ala Ile Glu Arg Met Glu
 30 35 40
 gaa gat cag gac ttg ctt tcc tat tat cag ctt atg aat ttt aga cat 677
 Glu Asp Gln Asp Leu Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His
 45 50 55
 gag tta atg ttg gaa tat ctt ttc ccg gca gaa aaa aag ctg agc aaa 725
 Glu Leu Met Leu Glu Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys
 60 65 70 75
 tct gat tat ctt agg gaa att gag gga cag gga aga aaa ttg tca ggc 773
 Ser Asp Tyr Leu Arg Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly
 80 85 90

10295.204.ST25.txt

ttg ctc gaa tac tat ttt tcc ttt ttc acc gga atg tat cat ttt tct	821
Leu Leu Glu Tyr Tyr Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser	
95 100 105	
cgc gga aaa tac ata aag gca atc aag gca tat aga gca gca gaa aaa	869
Arg Gly Lys Tyr Ile Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys	
110 115 120	
aag ttg acg aaa gtt tca gat aaa ata gaa aag gct gaa ttc tat tat	917
Lys Leu Thr Lys Val Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr	
125 130 135	
aag atg gcg gaa gtg ttt tat cat atg aaa cag act cat atg tca atg	965
Lys Met Ala Glu Val Phe Tyr His Met Lys Gln Thr His Met Ser Met	
140 145 150 155	
tat tat gtg tct ctc gct tat gat att tat aaa tcc tat gat gca tat	1013
Tyr Tyr Val Ser Leu Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr	
160 165 170	
gtg att cga aga att aat tgt cta ttc gtt gtt gct ggg aat tac att	1061
Val Ile Arg Arg Ile Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile	
175 180 185	
gat tta tca acc cat gat caa gct tta ccg cat ctt tta agc gct aag	1109
Asp Leu Ser Thr His Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys	
190 195 200	
gaa tcc gcg gaa gac att caa aac aag gcg atc gtt gca aag gct ctt	1157
Glu Ser Ala Glu Asp Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu	
205 210 215	
tta aat gta gca tat tgt tat aat gca atg gag aga cca aca aaa gct	1205
Leu Asn Val Ala Tyr Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala	
220 225 230 235	
att gaa tac ttt cat aag gcg att gat gta gca aag gaa ata aag gca	1253
Ile Glu Tyr Phe His Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala	
240 245 250	
aaa gaa ctg act cag gct tat tat gat ttg gca tta att cac ttt cga	1301
Lys Glu Leu Thr Gln Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg	
255 260 265	
aat aac gaa aat att gaa gga cga aaa ttt tat gaa aag gcg ctt gaa	1349
Asn Asn Glu Asn Ile Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu	
270 275 280	
agt gcg cgg gta ttt gaa gat gaa tta ttc ctg tgt ctg ttg gat gtt	1397
Ser Ala Arg Val Phe Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val	
285 290 295	
tta gag gca ctg ttt ata aaa tca gct aat aag tca gag gta cta gaa	1445
Leu Glu Ala Leu Phe Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu	
300 305 310 315	
aca atg aaa cca tta cgg gat agt cgt ggt tac ccc tat ctt gag gaa	1493
Thr Met Lys Pro Leu Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu	
320 325 330	
ctg gca tta gaa gca gct cta ttc tat act agg aat gag cgg cca aat	1541
Leu Ala Leu Glu Ala Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn	
335 340 345	
gat tcc ata ttt ttt tat gat cag atg gtg cag gct cag aaa caa atc	1589
Asp Ser Ile Phe Phe Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile	
350 355 360	

10295.204.ST25.txt

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aaa agg ggc gac ttt ctg tat gaa atc taagctgttt ctttcgctga      1636
Lys Arg Gly Asp Phe Leu Tyr Glu Ile
365                               370

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aacatgcaga attttctgta gcatctaggc tcgcaacata attgtgtttg ggcagggtcat 1756
gtgatggcct gccttttttg tgaaagaatt attttagttt gaaaaccaga acgattgtgt 1816
taatactcat ctttcttcgt cccttggtgtt ggaattttca tcatatcaat atttgaatat 1876
gcggctgtcc gcattattaa caattttaaa tttttgcac aaattttata caaaggcaga 1936
caaaaacctt gatatatcaa tggttctatg ggtatattca accacgacca ccgatatcgc 1996
taaaaaccgt attgccaaac gacgaaagag cgttccttac acaaggaatg ctctttttgt 2056
ttattcctca tcaaagcgga gagccgcaa cataaacgca atgaccaact gttgtccgca 2116

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<210> 155
 <211> 372
 <212> PRT
 <213> Bacillus licheniformis

<400> 155

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Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu Ala Glu Arg Leu Lys
 20 25 30

Ala Glu Val His Leu Ala Ile Glu Arg Met Glu Glu Asp Gln Asp Leu
 35 40 45

Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His Glu Leu Met Leu Glu
 50 55 60

Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys Ser Asp Tyr Leu Arg
 65 70 75 80

Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly Leu Leu Glu Tyr Tyr
 85 90 95

Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser Arg Gly Lys Tyr Ile
 100 105 110

Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys Lys Leu Thr Lys Val
 115 120 125

Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr Lys Met Ala Glu Val
 130 135 140

Phe Tyr His Met Lys Gln Thr His Met Ser Met Tyr Tyr Val Ser Leu
 145 150 155 160

10295.204.ST25.txt

Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr Val Ile Arg Arg Ile
165 170 175

Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile Asp Leu Ser Thr His
180 185 190

Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys Glu Ser Ala Glu Asp
195 200 205

Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu Leu Asn Val Ala Tyr
210 215 220

Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala Ile Glu Tyr Phe His
225 230 235 240

Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala Lys Glu Leu Thr Gln
245 250 255

Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg Asn Asn Glu Asn Ile
260 265 270

Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu Ser Ala Arg Val Phe
275 280 285

Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val Leu Glu Ala Leu Phe
290 295 300

Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu Thr Met Lys Pro Leu
305 310 315 320

Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu Leu Ala Leu Glu Ala
325 330 335

Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn Asp Ser Ile Phe Phe
340 345 350

Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile Lys Arg Gly Asp Phe
355 360 365

Leu Tyr Glu Ile
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<210> 156
<211> 1576
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1268)
<400> 156

10295.204.S125.txt																		
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caagcttcac	aaaaccggtc	gatgccggag	aaatcgaaga	aaagctggac	acttcacacg													180
gcatgattcg	gactgaggtg	agaagcaagt	ctgccgattc	ccatctttgga	cacgtgtttc													240
cggacggacc	cggaccggac	ggcctgcgct	attgcatcaa	ttcagccgcc	ctccggtttg													300
tgccgaagga	cgaccttgag	aaagaaggat	acggcgaata	tgtcaaactg	tttgaacgca													360
agaaatccgg	agaggaaagc	tgaggagagc	agcatgcaag	atgatacctt	tttcaaaggg													420
tcatactttt	ttagaggatt	ttctgctctg	aaagcgaaaa	aacattacaa	tagatcatct													480
tgagaaaaga	ggcagccgtt	gtg	aca	tcc	att	tca	aac	aca	gaa	gac	cgt	tat						533
		Val	Thr	Ser	Ile	Ser	Asn	Thr	Glu	Asp	Arg	Tyr						
		1				5					10							
tta	atg	ctg	aca	tgc	agc	aaa	aaa	att	gaa	tcc	cat	tat	cat	ata	tac			581
Leu	Met	Leu	Thr	Cys	Ser	Lys	Lys	Ile	Glu	Ser	His	Tyr	His	Ile	Tyr			
			15					20					25					
aca	gat	gag	gag	atc	ccg	cag	atg	ttt	tcc	tct	cat	ttt	ctg	cag	ctg			629
Thr	Asp	Glu	Glu	Ile	Pro	Gln	Met	Phe	Ser	Ser	His	Phe	Leu	Gln	Leu			
		30					35					40						
cag	gac	gat	ttt	ccg	ctg	aca	gag	ctg	tac	tcc	ctg	ctc	gtt	cgg	aca			677
Gln	Asp	Asp	Phe	Pro	Leu	Thr	Glu	Leu	Tyr	Ser	Leu	Leu	Val	Arg	Thr			
		45				50					55							
ccc	gaa	att	tta	aaa	cga	aat	tat	gtt	cat	gtg	aaa	agc	tct	tat	aag			725
Pro	Glu	Ile	Leu	Lys	Arg	Asn	Tyr	Val	His	Val	Lys	Ser	Ser	Tyr	Lys			
					65					70					75			
cgg	gat	ctg	cct	ttt	acg	atg	aaa	aag	tcg	ctc	ttt	gat	ctt	ggc	tat			773
Arg	Asp	Leu	Pro	Phe	Thr	Met	Lys	Lys	Ser	Leu	Phe	Asp	Leu	Gly	Tyr			
				80					85					90				
att	ctt	gat	gaa	gaa	ttg	ttt	tat	tcc	atc	agg	ctt	gca	gat	tgg	aaa			821
Ile	Leu	Asp	Glu	Glu	Leu	Phe	Tyr	Ser	Ile	Arg	Leu	Ala	Asp	Trp	Lys			
			95					100					105					
gga	gat	tcc	cct	ggt	gta	cgg	gca	gag	tgg	ggg	acg	gag	aaa	tcg	ctc			869
Gly	Asp	Ser	Pro	Gly	Val	Arg	Ala	Glu	Trp	Gly	Thr	Glu	Lys	Ser	Leu			
		110					115					120						
att	gac	ggc	tgc	cgc	atg	atg	cag	gct	tat	gat	aca	ttg	tct	atc	aat			917
Ile	Asp	Gly	Cys	Arg	Met	Met	Gln	Ala	Tyr	Asp	Thr	Leu	Ser	Ile	Asn			
		125				130					135							

10295.204.ST25.txt

```

tcg ggc ctt atc aag cag atg ctc acc gcc gcc aaa caa tcg ggc atg      1157
Ser Gly Leu Ile Lys Gln Met Leu Thr Ala Ala Lys Gln Ser Gly Met
205                               210                               215

gaa tcg tgc tat ctt gta act tcg gga agc gat cag gtg aaa acg ttt      1205
Glu Ser Cys Tyr Leu Val Thr Ser Gly Ser Asp Gln Val Lys Thr Phe
220                               225                               230                               235

tat gaa aag ctg ggc ttt cag cag aag gaa aag ctc acg aca ata ttt      1253
Tyr Glu Lys Leu Gly Phe Gln Gln Lys Glu Lys Leu Thr Thr Ile Phe
240                               245                               250

aaa tat ttg ttc gta taaagtaggc aggtgcacat accaattggg acttggcctg      1308
Lys Tyr Leu Phe Val

cataggctgg ggtgtagact ttatacgaaa ggatgataag cctgtgcatt actcccatta      1368
ttgctgtcct actggaggat acggctacgg gtttcacgga agaacacatt tgactcatcg      1428
ttgtcctctt tattttgctc atcattgtcg gtgcggcttt catttgctag ctaaaagccc      1488
gacgcccggc gcttgacatg ctcacaaagc cttcctccgg aagggtttttt ttgggtttttg      1548
ttggaaaatt ttgcattcgt atgtaata      1576

```

<210> 157

<211> 256

<212> PRT

<213> Bacillus licheniformis

<400> 157

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Val Thr Ser Ile Ser Asn Thr Glu Asp Arg Tyr Leu Met Leu Thr Cys
1          5          10          15

```

```

Ser Lys Lys Ile Glu Ser His Tyr His Ile Tyr Thr Asp Glu Glu Ile
20          25          30

```

```

Pro Gln Met Phe Ser Ser His Phe Leu Gln Leu Gln Asp Asp Phe Pro
35          40          45

```

```

Leu Thr Glu Leu Tyr Ser Leu Leu Val Arg Thr Pro Glu Ile Leu Lys
50          55          60

```

```

Arg Asn Tyr Val His Val Lys Ser Ser Tyr Lys Arg Asp Leu Pro Phe
65          70          75          80

```

```

Thr Met Lys Lys Ser Leu Phe Asp Leu Gly Tyr Ile Leu Asp Glu Glu
85          90          95

```

```

Leu Phe Tyr Ser Ile Arg Leu Ala Asp Trp Lys Gly Asp Ser Pro Gly
100          105          110

```

```

Val Arg Ala Glu Trp Gly Thr Glu Lys Ser Leu Ile Asp Gly Cys Arg
115          120          125

```

```

Met Met Gln Ala Tyr Asp Thr Leu Ser Ile Asn Glu Ala Phe Ala Lys
130          135          140

```

10295.204.ST25.txt

Glu Lys Leu Leu Arg Lys Tyr Pro Phe Tyr Glu Glu Gly Ile Ile Gln
 145 150 155 160

Leu Cys Val Cys Tyr Ser Glu Glu Gly Glu Pro Ile Gly Cys Ala Glu
 165 170 175

Leu Tyr Leu Asp His Asp Glu Asn Val Ala Lys Ile Glu Glu Val Ala
 180 185 190

Ile Leu Glu Pro Tyr Gln Arg Lys Gly Tyr Gly Ser Gly Leu Ile Lys
 195 200 205

Gln Met Leu Thr Ala Ala Lys Gln Ser Gly Met Glu Ser Cys Tyr Leu
 210 215 220

Val Thr Ser Gly Ser Asp Gln Val Lys Thr Phe Tyr Glu Lys Leu Gly
 225 230 235 240

Phe Gln Gln Lys Glu Lys Leu Thr Thr Ile Phe Lys Tyr Leu Phe Val
 245 250 255

<210> 158
 <211> 1783
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1283)

<400> 158
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 ttgagtttct ttttcacttt ttcgatcagc tcgtcttcat caggagctga cagcggacga 120
 ttattgacaa acgcaaacga tttttttcgt cccggccgc agtaagactg gcagccgatt 180
 tccacttttg catccggatc aatttctttc agacggggca aaagcgtctt taaattggtg 240
 gcctggcaat cgtcgcatatc tcgaaattca ttagccattt catagcttc ctttcgtttt 300
 gttcatctgt ctttatgaaa ggcattcaac tgtgccgaac ttttataaaa aatgacacca 360
 tccttcattt tacaaggatt ctttcattcc tgcaaggatc gcgctaataa aatcagttcc 420
 tattctttta gcaaacttgt ataaatattt tccaaaatgg acaatctaata accaataactg 480
 acaatgggag ttgagaagtg atg aaa caa aga caa gac gct tgg tct gag gaa 533
 Met Lys Gln Arg Gln Asp Ala Trp Ser Glu Glu
 1 5 10
 aat gat tta ctg ctt gct gaa acg gta ttg cgg cat gtc agg gaa ggg 581
 Asn Asp Leu Leu Leu Ala Glu Thr Val Leu Arg His Val Arg Glu Gly
 15 20 25
 agc aca cag ctg aac gcc ttc gag gaa gtc gga gac aga ctg aac agg 629
 Ser Thr Gln Leu Asn Ala Phe Glu Glu Val Gly Asp Arg Leu Asn Arg
 30 35 40

10295.204.ST25.txt

aca tca gcc gcc tgc ggt ttt aga tgg aac gca gtt gtc cgc cac caa	677
Thr Ser Ala Ala Cys Gly Phe Arg Trp Asn Ala Val Val Arg His Gln	
45 50 55	
tac gaa aaa gca ttg cag ctg gct aaa aaa cag agg aag caa aga atg	725
Tyr Glu Lys Ala Leu Gln Leu Ala Lys Lys Gln Arg Lys Gln Arg Met	
60 65 70 75	
cgc gcc ctc gga aac gga cag ccg gcg aaa aaa cgc tta tta tac aag	773
Arg Ala Leu Gly Asn Gly Gln Pro Ala Lys Lys Arg Leu Leu Tyr Lys	
80 85 90	
ccg ccg gtc gaa acg aat gct gaa cct cct gca gaa agc gtt gtt gag	821
Pro Pro Val Glu Thr Asn Ala Glu Pro Pro Ala Glu Ser Val Val Glu	
95 100 105	
cag aag aaa gca acc gca gat tca agc gaa cag cag ccg atc gcc agc	869
Gln Lys Lys Ala Thr Ala Asp Ser Ser Glu Gln Gln Pro Ile Ala Ser	
110 115 120	
gag cat ctg cct tat gtt gat gag agc ttt aaa gaa gag tta gct agt	917
Glu His Leu Pro Tyr Val Asp Glu Ser Phe Lys Glu Glu Leu Ala Ser	
125 130 135	
tta tct cac ctt cta tcg cca aat cag ccg cag gcc ggc cat aca gcc	965
Leu Ser His Leu Leu Ser Pro Asn Gln Pro Gln Ala Gly His Thr Ala	
140 145 150 155	
gat aca tcg aaa gac atg acg atc gat gat gtg atc cgc ttc ctg caa	1013
Asp Thr Ser Lys Asp Met Thr Ile Asp Asp Val Ile Arg Phe Leu Gln	
160 165 170	
aac tat aca gga aac gaa gaa caa act gcc gct tta aaa atg gaa aat	1061
Asn Tyr Thr Gly Asn Glu Glu Gln Thr Ala Ala Leu Lys Met Glu Asn	
175 180 185	
gaa cgt tta aaa cag gaa aac gaa gaa ctg acg aag aaa gtt gaa aag	1109
Glu Arg Leu Lys Gln Glu Asn Glu Glu Leu Thr Lys Lys Val Glu Lys	
190 195 200	
ctt gaa gcg gaa gtc aaa aag ctg gaa aaa gac cag aca acc atc cag	1157
Leu Glu Ala Glu Val Lys Lys Leu Glu Lys Asp Gln Thr Thr Ile Gln	
205 210 215	
gaa gac tac gaa acg ctc gta aaa att atg aac cgt gca aga aaa cta	1205
Glu Asp Tyr Glu Thr Leu Val Lys Ile Met Asn Arg Ala Arg Lys Leu	
220 225 230 235	
gtt tta ttc gaa gaa gac gaa cac gct gcg ccc gcc ttc aaa atg gac	1253
Val Leu Phe Glu Glu Asp Glu His Ala Ala Pro Ala Phe Lys Met Asp	
240 245 250	
cgg aac ggc aat tta gaa aaa atg gct gaa tagcgctctc agaggatgcg	1303
Arg Asn Gly Asn Leu Glu Lys Met Ala Glu	
255 260	
gcagagacgt tcaggcagca aggactgaca atgcatacaa acatttttcg atacgaggat	1363
accccttttct ttaaaaaagg gggtattttt accttttctgc ggcttgcttt tatatgacaa	1423
aaatttcata atagggatag caattcataa ggcgggggtat tcgatgaagt ttgttttata	1483
tgccggttcag ttccgacctg cggccctttt gtttttgttt tctgcattgg caagctggta	1543
tcaaggcagc gagcttttta aggtgccgtg ggagtggaaa tatacagcca agttttacaag	1603
ttggctgtac ggagaggact ccattaaaaa cgcacataat atttcacagc ttgatttttt	1663

10295.204.ST25.txt

cgtctatgcg gccaaagcata cgccggcaac cgttatttta atggccgtca gtttggcgta 1723
 tatcatcgct ttggcggcctt atcttctcat caaaacatat gtaaaacgaa aaagcgcttc 1783

<210> 159
 <211> 261
 <212> PRT
 <213> Bacillus licheniformis

<400> 159

Met Lys Gln Arg Gln Asp Ala Trp Ser Glu Glu Asn Asp Leu Leu Leu
 1 5 10 15

Ala Glu Thr Val Leu Arg His Val Arg Glu Gly Ser Thr Gln Leu Asn
 20 25 30

Ala Phe Glu Glu Val Gly Asp Arg Leu Asn Arg Thr Ser Ala Ala Cys
 35 40 45

Gly Phe Arg Trp Asn Ala Val Val Arg His Gln Tyr Glu Lys Ala Leu
 50 55 60

Gln Leu Ala Lys Lys Gln Arg Lys Gln Arg Met Arg Ala Leu Gly Asn
 65 70 75 80

Gly Gln Pro Ala Lys Lys Arg Leu Leu Tyr Lys Pro Pro Val Glu Thr
 85 90 95

Asn Ala Glu Pro Pro Ala Glu Ser Val Val Glu Gln Lys Lys Ala Thr
 100 105 110

Ala Asp Ser Ser Glu Gln Gln Pro Ile Ala Ser Glu His Leu Pro Tyr
 115 120 125

Val Asp Glu Ser Phe Lys Glu Glu Leu Ala Ser Leu Ser His Leu Leu
 130 135 140

Ser Pro Asn Gln Pro Gln Ala Gly His Thr Ala Asp Thr Ser Lys Asp
 145 150 155 160

Met Thr Ile Asp Asp Val Ile Arg Phe Leu Gln Asn Tyr Thr Gly Asn
 165 170 175

Glu Glu Gln Thr Ala Ala Leu Lys Met Glu Asn Glu Arg Leu Lys Gln
 180 185 190

Glu Asn Glu Glu Leu Thr Lys Lys Val Glu Lys Leu Glu Ala Glu Val
 195 200 205

Lys Lys Leu Glu Lys Asp Gln Thr Thr Ile Gln Glu Asp Tyr Glu Thr
 210 215 220

Leu Val Lys Ile Met Asn Arg Ala Arg Lys Leu Val Leu Phe Glu Glu
225 230 235 240

Asp Glu His Ala Ala Pro Ala Phe Lys Met Asp Arg Asn Gly Asn Leu
245 250 255

Glu Lys Met Ala Glu
260

<210> 160
<211> 2311
<212> DNA
<213> *Bacillus licheniformis*

<220>
<221> CDS
<222> (501) .. (1811)

[illegible]

10295.204.ST25.txt

gaa gct gaa ata gct gct ttt ttg agc aaa aag cat gtc atg gct tca Glu Ala Glu Ile Ala Ala Phe Leu Ser Lys Lys His Val Met Ala Ser 110 115 120	869
tcc agc gga acc gat gcc atg att gtc gcg ctg aag gct gcg ggt gtt Ser Ser Gly Thr Asp Ala Met Ile Val Ala Leu Lys Ala Ala Gly Val 125 130 135	917
gga caa ggt gat gaa gtc att atg cct gca aac agc ttt gct gca acg Gly Gln Gly Asp Glu Val Ile Met Pro Ala Asn Ser Phe Ala Ala Thr 140 145 150 155	965
gaa aac gcc gtg ctc gca gct gga ggc act ccg att ttc tgc gat att Glu Asn Ala Val Leu Ala Ala Gly Gly Thr Pro Ile Phe Cys Asp Ile 160 165 170	1013
gac cct gtt aca ttt tgc atg gat cct tca gaa att gaa gca tgt gtc Asp Pro Val Thr Phe Cys Met Asp Pro Ser Glu Ile Glu Ala Cys Val 175 180 185	1061
act ttg aaa acg aaa tgc att ttg cct gta cac ctt tat gga aag ctg Thr Leu Lys Thr Lys Cys Ile Leu Pro Val His Leu Tyr Gly Lys Leu 190 195 200	1109
cct gac atg gaa gcc att gca aaa acc gct gat aaa tac ggc atc ccg Pro Asp Met Glu Ala Ile Ala Lys Thr Ala Asp Lys Tyr Gly Ile Pro 205 210 215	1157
att att gaa gac gcc tgc cag gcg atc ggc gtt tcc gat ctg gga aaa Ile Ile Glu Asp Ala Cys Gln Ala Ile Gly Val Ser Asp Leu Gly Lys 220 225 230 235	1205
aac agc ctt tgc tcc ata tta agc ttc aat ccg tat aaa aat ctc ggc Asn Ser Leu Cys Ser Ile Leu Ser Phe Asn Pro Tyr Lys Asn Leu Gly 240 245 250	1253
act tgc gga aaa gcc ggc gca att gtg acg gat gat cca tca ttt gca Thr Cys Gly Lys Ala Gly Ala Ile Val Thr Asp Asp Pro Ser Phe Ala 255 260 265	1301
tcc gca tgc atg gaa tat atg tat cac ggc ttt gaa ctg aat caa aaa Ser Ala Cys Met Glu Tyr Met Tyr His Gly Phe Glu Leu Asn Gln Lys 270 275 280	1349
aat aaa aag gcg gct gac tac ggc ttt aac gct aag att gat aat ctg Asn Lys Lys Ala Ala Asp Tyr Gly Phe Asn Ala Lys Ile Asp Asn Leu 285 290 295	1397
caa gcc gct att gga ctg gca agg atg aaa tat ctt tct tta aat aat Gln Ala Ala Ile Gly Leu Ala Arg Met Lys Tyr Leu Ser Leu Asn Asn 300 305 310 315	1445
ctg aag cgc tta tat tta gca gat cgt tat att gcg cat ttg cag cag Leu Lys Arg Leu Tyr Leu Ala Asp Arg Tyr Ile Ala His Leu Gln Gln 320 325 330	1493
tat gaa gac aga ggt ctg atc aaa ttg cct caa atg acc gat gat cat Tyr Glu Asp Arg Gly Leu Ile Lys Leu Pro Gln Met Thr Asp Asp His 335 340 345	1541
gta tgg cat ttg ttt aca att aaa ata cta aac gga aat cgt gac caa Val Trp His Leu Phe Thr Ile Lys Ile Leu Asn Gly Asn Arg Asp Gln 350 355 360	1589
gtc aaa gat atg atg ctt aaa ttt cat aat gtc caa aca gat ata tac Val Lys Asp Met Met Leu Lys Phe His Asn Val Gln Thr Asp Ile Tyr 365 370 375	1637

10295.204.ST25.txt

tac ccg att tta tcc cat cat caa aac aca cca ctt gta aaa gcc aat 1685
 Tyr Pro Ile Leu Ser His His Gln Asn Thr Pro Leu Val Lys Ala Asn 395
 380 385 390

tat cgg cac aca tca ctg ccg gtc act gaa tca gtg cat aaa caa atg 1733
 Tyr Arg His Thr Ser Leu Pro Val Thr Glu Ser Val His Lys Gln Met 410
 400 405

ctt cag ctt cct ctc tat ccg ggg ctc acc gta gaa gaa caa gac aaa 1781
 Leu Gln Leu Pro Leu Tyr Pro Gly Leu Thr Val Glu Glu Gln Asp Lys 425
 415 420

gta atg gag gcc tta att gat gtc gta tca tgaacactt tcttttcaca 1831
 Val Met Glu Ala Leu Ile Asp Val Val Ser 435
 430

ccttgcagca agtaaacaag ccgaagtacg ccgtattttg cgattttgat gagacatatt 1891

tcgcccacag catcaccgat gaatcgagaa aagcgctcat ggaccttgaa acattttattc 1951

attcgcacca tcttgatcac aagattttgc tcggctgggt gaccgggagc agcctgtcat 2011

ccgttcttgc aaaaatgaag cggggaggct ttcgatatct tccgcatttt gtcgccggtg 2071

accttggcac tgaaatcact tatttctctg aagaaggcca agtctctgat aaagattggg 2131

aagcccgatt gcaagaatca aatttctccc atgatctggt cgaagaaatc aagcagactc 2191

tctctaaaaa atatgagatt gcgcttgtgc ctcagactca gcatggcttt tcccgtata 2251

aaatcaacta ttactataaa tcgttggaag agagcataga taagagggcg cttgaagcca 2311

<210> 161

<211> 437

<212> PRT

<213> Bacillus licheniformis

<400> 161

Met Lys Thr Ala Asn Glu Asn Met Thr Cys Thr Ser Lys Gln Leu Phe
 1 5 10 15

Val Leu Leu Asn Asp Leu Lys Glu Gly Lys Leu Ala Gly Glu Cys Arg
 20 25 30

Ile Asp Asp Thr Leu Ala Asn Gln Lys Leu Lys Glu Thr Leu Gln Gln
 35 40 45

Asp Gln Phe Asp Ile Thr Ala Asn Leu Leu Asn Arg Met Asp Ser Pro
 50 55 60

Pro Ser Arg Val Asp Phe Met Pro Leu His Arg Leu Ile Thr Glu Glu
 65 70 75 80

Glu Val Asp Asp Val Val His Ala Val Lys Asp Val Leu Pro Thr Gly
 85 90 95

Gln Phe Thr Ser Gly Phe Tyr Val Gly Val Phe Glu Ala Glu Ile Ala
 100 105 110

10295.204.ST25.txt

Ala Phe Leu Ser Lys Lys His Val Met Ala Ser Ser Ser Gly Thr Asp
 115 120 125

Ala Met Ile Val Ala Leu Lys Ala Ala Gly Val Gly Gln Gly Asp Glu
 130 135 140

Val Ile Met Pro Ala Asn Ser Phe Ala Ala Thr Glu Asn Ala Val Leu
 145 150 155 160

Ala Ala Gly Gly Thr Pro Ile Phe Cys Asp Ile Asp Pro Val Thr Phe
 165 170 175

Cys Met Asp Pro Ser Glu Ile Glu Ala Cys Val Thr Leu Lys Thr Lys
 180 185 190

Cys Ile Leu Pro Val His Leu Tyr Gly Lys Leu Pro Asp Met Glu Ala
 195 200 205

Ile Ala Lys Thr Ala Asp Lys Tyr Gly Ile Pro Ile Ile Glu Asp Ala
 210 215 220

Cys Gln Ala Ile Gly Val Ser Asp Leu Gly Lys Asn Ser Leu Cys Ser
 225 230 235 240

Ile Leu Ser Phe Asn Pro Tyr Lys Asn Leu Gly Thr Cys Gly Lys Ala
 245 250 255

Gly Ala Ile Val Thr Asp Asp Pro Ser Phe Ala Ser Ala Cys Met Glu
 260 265 270

Tyr Met Tyr His Gly Phe Glu Leu Asn Gln Lys Asn Lys Lys Ala Ala
 275 280 285

Asp Tyr Gly Phe Asn Ala Lys Ile Asp Asn Leu Gln Ala Ala Ile Gly
 290 295 300

Leu Ala Arg Met Lys Tyr Leu Ser Leu Asn Asn Leu Lys Arg Leu Tyr
 305 310 315 320

Leu Ala Asp Arg Tyr Ile Ala His Leu Gln Gln Tyr Glu Asp Arg Gly
 325 330 335

Leu Ile Lys Leu Pro Gln Met Thr Asp Asp His Val Trp His Leu Phe
 340 345 350

Thr Ile Lys Ile Leu Asn Gly Asn Arg Asp Gln Val Lys Asp Met Met
 355 360 365

Leu Lys Phe His Asn Val Gln Thr Asp Ile Tyr Tyr Pro Ile Leu Ser
 370 375 380

10295.204.ST25.txt

His His Gln Asn Thr Pro Leu Val Lys Ala Asn Tyr Arg His Thr Ser
385 390 395 400

Leu Pro Val Thr Glu Ser Val His Lys Gln Met Leu Gln Leu Pro Leu
405 410 415

Tyr Pro Gly Leu Thr Val Glu Glu Gln Asp Lys Val Met Glu Ala Leu
420 425 430

Ile Asp Val Val Ser
435

<210> 162
<211> 2143
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1643)

<400> 162
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caaaacagca tcagacagca gctgtatgaa cgcattgggtc ttccgcttga ccggtatgcg 120
gttttgattc atccctctgc tggtgtcagc ggttcggccc ggattcaaaa cggcgccggtt 180
gttatggcat cgagcgtcat ccaagcggat gcagacgtcg gcatccacgc gattgtcaac 240
acaggtgcga tcgtcgaaca cgacaatcgg atcggcgatt acgttcatct ttcgcccgga 300
acggtgttaa ccggcggcgt gacagttatg gaaggcgctc atctcggcgc gggaacggcg 360
gtcattcccc gaaagacagt cggacgctgg agcgtgacgg gagcgggggc agccgtgatt 420
cacgacattc ctgataattg caccgcagtc ggagtccttg caagaatgat caaataacag 480
cagtaaaaag ggtgaaaaac atg agt cag aat aag cga att tat tta tca ccg 533
Met Ser Gln Asn Lys Arg Ile Tyr Leu Ser Pro 10
1 5
ccg cac atg agc gga gac gag gag cgc tat gta gcc gaa gcg ttt cgg 581
Pro His Met Ser Gly Asp Glu Glu Arg Tyr Val Ala Glu Ala Phe Arg 15 20 25
aca aac tgg atc gcg ccc ctc ggt ccc ctt gtc gac aca ttt gaa gaa 629
Thr Asn Trp Ile Ala Pro Leu Gly Pro Leu Val Asp Thr Phe Glu Glu 30 35 40
aag ctt gcc gcc tat gcg ggg acg tcc gga gcc gcg gca gtc agc tca 677
Lys Leu Ala Ala Tyr Ala Gly Thr Ser Gly Ala Ala Ala Val Ser Ser 45 50 55
gga aca gct gcg atc cac ctg gcc ttg aaa ttg ctc ggc gtc ggc aaa 725
Gly Thr Ala Ala Ile His Leu Ala Leu Lys Leu Leu Gly Val Gly Lys 60 65 70 75
ggc gat acg gtc ttc tgc tct tct ttt acg ttt gta gcg agc gcc aat 773
Gly Asp Thr Val Phe Cys Ser Ser Phe Thr Phe Val Ala Ser Ala Asn 80 85 90
ccg atc ata tat gag cag gct gaa ccg gtt ttc att gat tct gaa ccg 821

10295.204.ST25.txt

Pro	Ile	Ile	Tyr	Glu	Gln	Ala	Glu	Pro	Val	Phe	Ile	Asp	Ser	Glu	Arg		
			95					100					105				
gat	aca	tgg	aac	atg	tcg	ccc	gag	gcg	ctt	gaa	cgg	gcg	ctt	gac	gaa		869
Asp	Thr	Trp	Asn	Met	Ser	Pro	Glu	Ala	Leu	Glu	Arg	Ala	Leu	Asp	Glu		
		110					115					120					
gcg	gag	cgg	gcc	agg	aat	ctc	ccg	aaa	gcc	gtc	atc	gtc	gtc	aac	ttg		917
Ala	Glu	Arg	Ala	Arg	Asn	Leu	Pro	Lys	Ala	Val	Ile	Val	Val	Asn	Leu		
		125				130					135						
tac	ggc	caa	agc	gcg	aaa	atg	gac	gag	att	atg	gcc	att	tgc	gat	cga		965
Tyr	Gly	Gln	Ser	Ala	Lys	Met	Asp	Glu	Ile	Met	Ala	Ile	Cys	Asp	Arg		
		140			145					150					155		
ttt	gcc	gtg	cct	gtc	att	gaa	gat	gca	gcc	gaa	tcg	ctc	ggg	tct	gtt		1013
Phe	Ala	Val	Pro	Val	Ile	Glu	Asp	Ala	Ala	Glu	Ser	Leu	Gly	Ser	Val		
				160					165					170			
tat	aaa	ggc	aga	aaa	agc	ggg	acc	ttc	gga	cgc	ttc	ggc	att	tat	tcg		1061
Tyr	Lys	Gly	Arg	Lys	Ser	Gly	Thr	Phe	Gly	Arg	Phe	Gly	Ile	Tyr	Ser		
			175					180					185				
ttc	aac	ggg	aac	aaa	atc	atc	acc	aca	tcg	ggc	gga	gga	atg	ctg	gtc		1109
Phe	Asn	Gly	Asn	Lys	Ile	Ile	Thr	Thr	Ser	Gly	Gly	Gly	Met	Leu	Val		
		190					195					200					
agc	gat	gat	gaa	gac	gcg	ttg	aag	aag	gcg	cgc	ttt	tta	gcc	act	cag		1157
Ser	Asp	Asp	Glu	Asp	Ala	Leu	Lys	Lys	Ala	Arg	Phe	Leu	Ala	Thr	Gln		
		205				210					215						
gcg	cgc	gag	cca	gcc	att	cat	tat	cag	cac	gaa	aaa	gcg	ggc	tac	aat		1205
Ala	Arg	Glu	Pro	Ala	Ile	His	Tyr	Gln	His	Glu	Lys	Ala	Gly	Tyr	Asn		
				220		225				230					235		
tac	cgg	atg	agc	aat	gtt	ctg	gcc	gga	atc	ggc	atc	gca	cag	ctc	gcc		1253
Tyr	Arg	Met	Ser	Asn	Val	Leu	Ala	Gly	Ile	Gly	Ile	Ala	Gln	Leu	Ala		
				240					245					250			
gtt	ctg	gat	gac	cgg	gta	cat	gcc	aga	cgg	gcg	gtt	ttc	gag	cgc	tat		1301
Val	Leu	Asp	Asp	Arg	Val	His	Ala	Arg	Arg	Ala	Val	Phe	Glu	Arg	Tyr		
			255				260						265				
aag	gag	gcg	ctt	tcc	ggg	atc	gaa	ggg	ata	gaa	ttc	atg	cct	gag	gcc		1349
Lys	Glu	Ala	Leu	Ser	Gly	Ile	Glu	Gly	Ile	Glu	Phe	Met	Pro	Glu	Ala		
		270				275						280					
ggc	atg	tca	aac	cgc	tgg	ctc	acg	aca	tta	acg	tta	gac	aca	gca	aag		1397
Gly	Met	Ser	Asn	Arg	Trp	Leu	Thr	Thr	Leu	Thr	Leu	Asp	Thr	Ala	Lys		
		285				290					295						
att	caa	aca	aca	ccg	gcg	gac	atc	atc	gaa	cag	ctc	gca	aac	gaa	aac		1445
Ile	Gln	Thr	Thr	Pro	Ala	Asp	Ile	Ile	Glu	Gln	Leu	Ala	Asn	Glu	Asn		
				300		305				310				315			
att	gag	gcc	cgc	ccg	tta	tgg	aag	cct	ttg	cac	aga	cag	ccc	ctt	ttt		1493
Ile	Glu	Ala	Arg	Pro	Leu	Trp	Lys	Pro	Leu	His	Arg	Gln	Pro	Leu	Phe		
				320					325					330			
aaa	ggc	gcg	gcc	ttt	tat	ccg	cac	gat	gac	cag	ggc	tct	gtc	tgc	tgc		1541
Lys	Gly	Ala	Ala	Phe	Tyr	Pro	His	Asp	Asp	Gln	Gly	Ser	Val	Cys	Cys		
			335					340					345				
gac	tta	ttt	cag	cgc	ggg	ctc	tgc	ctg	ccg	tca	gga	tca	agt	atg	acg		1589
Asp	Leu	Phe	Gln	Arg	Gly	Leu	Cys	Leu	Pro	Ser	Gly	Ser	Ser	Met	Thr		
		350				355						360					
cga	aaa	gag	cag	gac	cgg	gta	att	caa	atc	gtt	gcc	gac	cgg	att	aaa		1637

10295.204.ST25.txt

Arg Lys Glu Gln Asp Arg Val Ile Gln Ile Val Ala Asp Arg Ile Lys
 365 370 375

tat aaa tgagggtgcta aacatggcga ttacatatc catggacagc ttaaagcata 1693
 Tyr Lys
 380

agctggcaga aattttggat gtcattccaa ggcattcatc agtcgtttac ttggactacc 1753
 cgctatacgg aaacgtcggg gatctattga tcatgaaagg aacggaagct ttttttgaag 1813
 catacggcat caagggtcgc gaaagatgga atgcggagaa tttcattccg ggccgccgca 1873
 ttccaaagga cgccatcatt gtttgtcagg ggggaggcaa tttcggcgac ttgtaccctc 1933
 acttccagca gttcagagaa cgggtggtcg aacattaccc ggacaaccgg atcgtcattc 1993
 tgccgcagtc gatttattat gagcatgaag aaaatataat aaaaacgcgc ggcattttgg 2053
 cggctcacc cggatctgcac ttattcacgc gggaaaaggc atcattcgat tttgccgtca 2113
 agcgtttcga agagggtgaaa aacatcaaaa 2143

<210> 163
 <211> 381
 <212> PRT
 <213> Bacillus licheniformis

<400> 163

Met Ser Gln Asn Lys Arg Ile Tyr Leu Ser Pro Pro His Met Ser Gly
 1 5 10 15

Asp Glu Glu Arg Tyr Val Ala Glu Ala Phe Arg Thr Asn Trp Ile Ala
 20 25 30

Pro Leu Gly Pro Leu Val Asp Thr Phe Glu Glu Lys Leu Ala Ala Tyr
 35 40 45

Ala Gly Thr Ser Gly Ala Ala Ala Val Ser Ser Gly Thr Ala Ala Ile
 50 55 60

His Leu Ala Leu Lys Leu Leu Gly Val Gly Lys Gly Asp Thr Val Phe
 65 70 75 80

Cys Ser Ser Phe Thr Phe Val Ala Ser Ala Asn Pro Ile Ile Tyr Glu
 85 90 95

Gln Ala Glu Pro Val Phe Ile Asp Ser Glu Arg Asp Thr Trp Asn Met
 100 105 110

Ser Pro Glu Ala Leu Glu Arg Ala Leu Asp Glu Ala Glu Arg Ala Arg
 115 120 125

Asn Leu Pro Lys Ala Val Ile Val Val Asn Leu Tyr Gly Gln Ser Ala
 130 135 140

Lys Met Asp Glu Ile Met Ala Ile Cys Asp Arg Phe Ala Val Pro Val
 Page 234

10295.204.ST25.txt

145

150

155

160

Ile Glu Asp Ala Ala Glu Ser Leu Gly Ser Val Tyr Lys Gly Arg Lys
 165 170 175

Ser Gly Thr Phe Gly Arg Phe Gly Ile Tyr Ser Phe Asn Gly Asn Lys
 180 185 190

Ile Ile Thr Thr Ser Gly Gly Gly Met Leu Val Ser Asp Asp Glu Asp
 195 200 205

Ala Leu Lys Lys Ala Arg Phe Leu Ala Thr Gln Ala Arg Glu Pro Ala
 210 215 220

Ile His Tyr Gln His Glu Lys Ala Gly Tyr Asn Tyr Arg Met Ser Asn
 225 230 235 240

Val Leu Ala Gly Ile Gly Ile Ala Gln Leu Ala Val Leu Asp Asp Arg
 245 250 255

Val His Ala Arg Arg Ala Val Phe Glu Arg Tyr Lys Glu Ala Leu Ser
 260 265 270

Gly Ile Glu Gly Ile Glu Phe Met Pro Glu Ala Gly Met Ser Asn Arg
 275 280 285

Trp Leu Thr Thr Leu Thr Leu Asp Thr Ala Lys Ile Gln Thr Thr Pro
 290 295 300

Ala Asp Ile Ile Glu Gln Leu Ala Asn Glu Asn Ile Glu Ala Arg Pro
 305 310 315 320

Leu Trp Lys Pro Leu His Arg Gln Pro Leu Phe Lys Gly Ala Ala Phe
 325 330 335

Tyr Pro His Asp Asp Gln Gly Ser Val Cys Cys Asp Leu Phe Gln Arg
 340 345 350

Gly Leu Cys Leu Pro Ser Gly Ser Ser Met Thr Arg Lys Glu Gln Asp
 355 360 365

Arg Val Ile Gln Ile Val Ala Asp Arg Ile Lys Tyr Lys
 370 375 380

<210> 164
 <211> 2107
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1607)

[illegible]

10295.204.ST25.txt

190	195	200	
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ttc cat gac aaa atc ggt ttc aac agc cgt ctt gat gaa tta cac gcc Phe His Asp Lys Ile Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala 220 225 230 235			1205
gca gct tta ctc att ctt ctt gag aaa atc gac ggc tgg aat gaa caa Ala Ala Leu Leu Ile Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln 240 245 250			1253
aga aga aga gtg gcc agc cgc tac aga gaa ggt ttg aaa acg gcg gag Arg Arg Arg Val Ala Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu 255 260 265			1301
cac ctc aca ctg ccg gca gag aaa gag gac cgc aca cat atc tat cat His Leu Thr Leu Pro Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His 270 275 280			1349
ctc tat tgt atc ggc gcg aaa aac cgc gac tac atc ata caa tcg ctg Leu Tyr Cys Ile Gly Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu 285 290 295			1397
aaa gag cag gac att cat tca ggt gtg tat tat cct tgc tgc ctt cat Lys Glu Gln Asp Ile His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His 300 305 310 315			1445
ctg caa tcg gtc tat tct tca ctg cag tac aaa aaa ggc gat ttt cct Leu Gln Ser Val Tyr Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro 320 325 330			1493
ata gcc gag tcc ttg tcc gaa acc ctt ttc gcc att ccg atg gat cct Ile Ala Glu Ser Leu Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro 335 340 345			1541
ttt cta gcc gcc gag gaa caa gat cag att att tct gcg ctg ctg aaa Phe Leu Ala Ala Glu Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys 350 355 360			1589
aaa gga gga ggg gaa aag tgacggttca ttttggttta atcggtgctg Lys Gly Gly Glu Lys 365			1637
gctatatgtc aagaaaacat cttcaagcac tggccgagtg cgatgatgca aagttgtcgg			1697
ccgtcagtga ttgacaggaa gaaagaatga aggaagcggga agaatactat gcttccctcg			1757
ccggtgagga aagccgaatg acccgctatc cgcagtatca agcgctgctt tcagatccta			1817
aaattgaagc ggtcattatt gcggcggttt cgggactgca cgccgaaatg gccaaacatg			1877
cgctgctggc aggcaagcac gtcacgctcg aaaaaccgat gaccttgctca ttacgggatg			1937
ccgatgagct tatagaactg gcggagcaga acgggctgaa gctcatggctc tgccaccaga			1997
tgcgccaccg gccgatcatg aaaaaactga aggaacgat tgaggaagga aagctgggaa			2057
agatctactt gggcacggta tcgctccgct taaacaggctc ccccgcttat			2107

<210> 165
 <211> 369
 <212> PRT
 <213> Bacillus licheniformis

10295.204.ST25.txt

<400> 165

Met Ile Pro Leu Val Asn Leu Lys Arg Gln Phe Gln Thr Val Lys Gln
 1 5 10 15
 Asp Ile Leu Lys Glu Phe Glu His Val Leu Asp Ser Gly Gln Tyr Ile
 20 25 30
 Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg Ile Ala Glu Lys Leu
 35 40 45
 Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly Thr Asp Ala Leu Val
 50 55 60
 Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly Asp Glu Val Ile Thr
 65 70 75 80
 Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala Val Ser Arg Val Gly
 85 90 95
 Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu Thr Tyr Asn Leu Asp
 100 105 110
 Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala Thr Lys Ala Ile Ile
 115 120 125
 Pro Val His Ile Phe Gly Gln Pro Ala Asp Met Asp Glu Ile Met Glu
 130 135 140
 Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu Asp Ala Cys Gln Ala
 145 150 155 160
 Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly Ser Ile Gly Asp Ala
 165 170 175
 Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu Gly Thr Leu Gly Asp
 180 185 190
 Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala Ala Arg Gln Leu Arg
 195 200 205
 Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr Phe His Asp Lys Ile
 210 215 220
 Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala Ala Ala Leu Leu Ile
 225 230 235 240
 Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln Arg Arg Arg Val Ala
 245 250 255
 Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu His Leu Thr Leu Pro
 260 265 270

10295.204.ST25.txt

Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His Leu Tyr Cys Ile Gly
 275 280 285

Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu Lys Glu Gln Asp Ile
 290 300

His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His Leu Gln Ser Val Tyr
 305 310 315 320

Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro Ile Ala Glu Ser Leu
 325 330 335

Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro Phe Leu Ala Ala Glu
 340 345 350

Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys Lys Gly Gly Gly Glu
 355 360 365

Lys

<210> 166
 <211> 2092
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1592)

<400> 166
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 catccggaaa acatctatat cggagataac gtttatatcg gccatgacac gattttaaaa 120
 ggctattata agcatgacct gatcatcggt tcaaacagct ggatcgggca gcaatgtttt 180
 atacacgggtg ccggcggggt tacaatcgga gaatttgag gaattggtcc gaacgtccgg 240
 atacatgccg ctaccatac cgatcctgat aaacccgaca gtaccatttt gttttcgccg 300
 cttacattcg ctctattca tattgaagaa aactgcaaca tcgggatcgg tgcgtctatc 360
 ctagcaggcg ttacgatagg cgcccactcc aaaatcggag caaatgccgt cgtcaatcgc 420
 aatattcccc cgtacagcat agcagtaggc gtgccggcaa aggtgattaa aaaccgaaga 480
 atgaaagatg aggatctctc atg atc aga ttg atc gag ccg tat att aca ttt 533
 Met Ile Arg Leu Ile Glu Pro Tyr Ile Thr Phe
 1 5 10
 gaa gaa gtg caa gca gaa tta aag gag ata ttt tcc tct ggc atg ctg 581
 Glu Glu Val Gln Ala Glu Leu Lys Glu Ile Phe Ser Ser Gly Met Leu
 15 20 25
 aca aaa ggc cct tat gtc aga aca ttt gct gat cat atg aga cag tat 629
 Thr Lys Gly Pro Tyr Val Arg Thr Phe Ala Asp His Met Arg Gln Tyr
 30 35 40

10295.204.ST25.txt

gtc agt gca aag cat gct ttt tta aca aca tcg gca aca acg gct tta Val Ser Ala Lys His Ala Phe Leu Thr Thr Ser Ala Thr Thr Ala Leu 45 50 55	677
tcg atg tgc ctt aaa agc ctg aac gtg caa ccc gga gat gaa gta atc Ser Met Cys Leu Lys Ser Leu Asn Val Gln Pro Gly Asp Glu Val Ile 60 65 70 75	725
gtc tca gac ttc tcg ttc ccc gcc act gtc aat gta ata gaa gat tta Val Ser Asp Phe Ser Phe Pro Ala Thr Val Asn Val Ile Glu Asp Leu 80 85 90	773
gga gcc aag ccg gtt ttt gcc gat gtt gat ctt gaa aca ttt aac atg Gly Ala Lys Pro Val Phe Ala Asp Val Asp Leu Glu Thr Phe Asn Met 95 100 105	821
ctt cca gaa gaa ctg gaa agt caa atc acg tcc cgt aca aaa gcc gtt Leu Pro Glu Glu Leu Glu Ser Gln Ile Thr Ser Arg Thr Lys Ala Val 110 115 120	869
ctt ttt gta gat gct ctt gga aac ccg aca ggc atc acc aac att aag Leu Phe Val Asp Ala Leu Gly Asn Pro Thr Gly Ile Thr Asn Ile Lys 125 130 135	917
caa att tgt aag gag tac ggc tta ccc ctt gtg gat gat gcc gct tgt Gln Ile Cys Lys Glu Tyr Gly Leu Pro Leu Val Asp Asp Ala Ala Cys 140 145 150 155	965
gcg atc ggc agc agc gaa tac ggc tgt aaa tcc gga aaa att gcc gat Ala Ile Gly Ser Ser Glu Tyr Gly Cys Lys Ser Gly Lys Ile Ala Asp 160 165 170	1013
ctc acc tgt ttc agc ttt cac cca aga aag ctg ctt acg aca ggc gaa Leu Thr Cys Phe Ser Phe His Pro Arg Lys Leu Leu Thr Thr Gly Glu 175 180 185	1061
ggc ggg gca att aca acc gac cgg gaa gag ttg aaa gac tgg ctt tcg Gly Gly Ala Ile Thr Thr Asp Arg Glu Glu Leu Lys Asp Trp Leu Ser 190 195 200	1109
gtc aaa tta aac cat ggc gct gcc atc tct gac gga aaa ttg gat ttt Val Lys Leu Asn His Gly Ala Ala Ile Ser Asp Gly Lys Leu Asp Phe 205 210 215	1157
ata gat ttc ggc tac aac tac aga tta tcc gat atc caa gcc gct ctt Ile Asp Phe Gly Tyr Asn Tyr Arg Leu Ser Asp Ile Gln Ala Ala Leu 220 225 230 235	1205
gga att aaa cag ctc caa aaa ctt gat gac atc att cat cgg aga aac Gly Ile Lys Gln Leu Gln Lys Leu Asp Asp Ile Ile His Arg Arg Asn 240 245 250	1253
ctt cag cag aaa gca tat agt gaa cag ctt gaa ccc ctc gga ttc caa Leu Gln Gln Lys Ala Tyr Ser Glu Gln Leu Glu Pro Leu Gly Phe Gln 255 260 265	1301
agt caa aaa atc ggt cca gcc gtt gta cac aac ata caa tcc gcc gtt Ser Gln Lys Ile Gly Pro Ala Val Val His Asn Ile Gln Ser Ala Val 270 275 280	1349
ttc aaa gtt cca aaa aac atc gtt cgc gac gaa ttg att caa tat ttg Phe Lys Val Pro Lys Asn Ile Val Arg Asp Glu Leu Ile Gln Tyr Leu 285 290 295	1397
agc gac tgc cat ata gag tcg act ttc ggc act tat tgt tta agc ggc Ser Asp Cys His Ile Glu Ser Thr Phe Gly Thr Tyr Cys Leu Ser Gly 300 305 310 315	1445

10295.204.ST25.txt

act ccc tat tac cgc cgg aaa tac caa cag cta aaa tcg aat tct ctc 1493
 Thr Pro Tyr Tyr Arg Arg Lys Tyr Gln Gln Leu Lys Ser Asn Ser Leu
 320 325 330

ttt ctt gaa caa cat acg att acc ctc cct tgc cat gat gaa gtc gat 1541
 Phe Leu Glu Gln His Thr Ile Thr Leu Pro Cys His Asp Glu Val Asp
 335 340 345

tta gat cat gtg gtt tca gcc ata caa tca ttt atc aaa ttt aag gtt 1589
 Leu Asp His Val Val Ser Ala Ile Gln Ser Phe Ile Lys Phe Lys Val
 350 355 360

gat tagttcaaaa tatcccgttc acagagaata gtgaacggga tattttttat 1642
 Asp

tcttaataca agaataaaaa aacaggtagt aaaccataga tttaccacct gattcattca 1702

cataacaata cagcgaactt ccatgaaaaa aaacattcac ctgtagatta agagacagtt 1762

ggaccgagaa tatatgcaaa tctgttagaa tgaaaatgct agtggaatat tcgatgtttt 1822

tacaagcatc gtttaatat tggacagaca atgtgtaact ctcaattgta caattagttt 1882

tctttaaaga gaaactgctc cgcaagaaaa acctacggaa cagcttccta atgagaatat 1942

taattagaaa gtttttcgat ttggatatga ccgctgtttc ctgtagcaag agttaacgct 2002

aatccagtga cggcaatctg aatagtagaa gggacagcag taacttcaat catagcttct 2062

cccactaatg gagtacctac gctgattaaa 2092

<210> 167

<211> 364

<212> PRT

<213> Bacillus licheniformis

<400> 167

Met Ile Arg Leu Ile Glu Pro Tyr Ile Thr Phe Glu Glu Val Gln Ala
 1 5 10 15

Glu Leu Lys Glu Ile Phe Ser Ser Gly Met Leu Thr Lys Gly Pro Tyr
 20 25 30

Val Arg Thr Phe Ala Asp His Met Arg Gln Tyr Val Ser Ala Lys His
 35 40 45

Ala Phe Leu Thr Thr Ser Ala Thr Thr Ala Leu Ser Met Cys Leu Lys
 50 55 60

Ser Leu Asn Val Gln Pro Gly Asp Glu Val Ile Val Ser Asp Phe Ser
 65 70 75 80

Phe Pro Ala Thr Val Asn Val Ile Glu Asp Leu Gly Ala Lys Pro Val
 85 90 95

Phe Ala Asp Val Asp Leu Glu Thr Phe Asn Met Leu Pro Glu Glu Leu
 100 105 110

10295.204.ST25.txt

Glu Ser Gln Ile Thr Ser Arg Thr Lys Ala Val Leu Phe Val Asp Ala
 115 120 125
 Leu Gly Asn Pro Thr Gly Ile Thr Asn Ile Lys Gln Ile Cys Lys Glu
 130 135 140
 Tyr Gly Leu Pro Leu Val Asp Asp Ala Ala Cys Ala Ile Gly Ser Ser
 145 150 155 160
 Glu Tyr Gly Cys Lys Ser Gly Lys Ile Ala Asp Leu Thr Cys Phe Ser
 165 170 175
 Phe His Pro Arg Lys Leu Leu Thr Thr Gly Glu Gly Gly Ala Ile Thr
 180 185 190
 Thr Asp Arg Glu Glu Leu Lys Asp Trp Leu Ser Val Lys Leu Asn His
 195 200 205
 Gly Ala Ala Ile Ser Asp Gly Lys Leu Asp Phe Ile Asp Phe Gly Tyr
 210 215 220
 Asn Tyr Arg Leu Ser Asp Ile Gln Ala Ala Leu Gly Ile Lys Gln Leu
 225 230 235 240
 Gln Lys Leu Asp Asp Ile Ile His Arg Arg Asn Leu Gln Gln Lys Ala
 245 250 255
 Tyr Ser Glu Gln Leu Glu Pro Leu Gly Phe Gln Ser Gln Lys Ile Gly
 260 265 270
 Pro Ala Val Val His Asn Ile Gln Ser Ala Val Phe Lys Val Pro Lys
 275 280 285
 Asn Ile Val Arg Asp Glu Leu Ile Gln Tyr Leu Ser Asp Cys His Ile
 290 295 300
 Glu Ser Thr Phe Gly Thr Tyr Cys Leu Ser Gly Thr Pro Tyr Tyr Arg
 305 310 315 320
 Arg Lys Tyr Gln Gln Leu Lys Ser Asn Ser Leu Phe Leu Glu Gln His
 325 330 335
 Thr Ile Thr Leu Pro Cys His Asp Glu Val Asp Leu Asp His Val Val
 340 345 350
 Ser Ala Ile Gln Ser Phe Ile Lys Phe Lys Val Asp
 355 360

<210> 168
 <211> 1663
 <212> DNA

10295.204.ST25.txt

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1163)

<400> 168

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tggtttccgg ttcatacaaac acagctgctc ctctgatttt tcatcgggct gtcggcagcc	120
ggcattttttc cgtgcgccgt cactcttgcc tcgttggtg gaaagccttt tacagaggaa	180
atcacgagtc tcttcatttc gtccgcaagt ctgggaggag cgcttctttc attcttgatc	240
ggctgggcga ttgatgcaag cgcagccgct gtcttcccgt ttttgctggt cggcggattg	300
gggggcttgc tgctggcgat cagcgcggtg atttttttat ccggcctgca aaaaaacaag	360
cagagtcatt tggatatgta gatttattag gaagagatta caagcttagt aggatttttt	420
tcagcagccg tttaaaccgt tccatctttg accataatat tgctagaaaa ggttgaagaa	480
cgagaggaac ggtggggaaa atg aag aaa tca aac att gcc tgt atg tat att	533
Met Lys Lys Ser Asn Ile Ala Cys Met Tyr Ile	
1 5 10	
ttt ctt tta tta ata gga gcg ctt gca aat ctc acg acg gaa gag act	581
Phe Leu Leu Leu Ile Gly Ala Leu Ala Asn Leu Thr Thr Glu Glu Thr	
15 20 25	
gcc caa tca tca ggc ggg cag cct gcc gtg att cct gat gaa gcg att	629
Ala Gln Ser Ser Gly Gly Gln Pro Ala Val Ile Pro Asp Glu Ala Ile	
30 35 40	
cgg ctg cgg att ttg gca aac agc gac agc ggg agc gac cag agc gtc	677
Arg Leu Arg Ile Leu Ala Asn Ser Asp Ser Gly Ser Asp Gln Ser Val	
45 50 55	
aaa cgc aaa atc agg gat gag gtc aat aaa caa att acg aaa tgg gtg	725
Lys Arg Lys Ile Arg Asp Glu Val Asn Lys Gln Ile Thr Lys Trp Val	
60 65 70 75	
gaa aac ctg acc tcg gtt gag gaa gcg aga caa gtc atc agg tcg aag	773
Glu Asn Leu Thr Ser Val Glu Glu Ala Arg Gln Val Ile Arg Ser Lys	
80 85 90	
ctg cct gaa atc caa gag gtt gcc atg gat gtc atg aaa cgc gaa aat	821
Leu Pro Glu Ile Gln Glu Val Ala Met Asp Val Met Lys Arg Glu Asn	
95 100 105	
gtt cgg caa tcc gtg tct gtc cgt ttt gat cgt gtt tca ttt ccg aca	869
Val Arg Gln Ser Val Ser Val Arg Phe Asp Arg Val Ser Phe Pro Thr	
110 115 120	
aag cta tac ggc aat atg gtg tat ccg gcc gga gaa tat gag gct gtt	917
Lys Leu Tyr Gly Asn Met Val Tyr Pro Ala Gly Glu Tyr Glu Ala Val	
125 130 135	
tta att aca tta ggc aag gga gag gga gcc aac tgg tgg tgc gtc ctg	965
Leu Ile Thr Leu Gly Lys Gly Glu Gly Ala Asn Trp Trp Cys Val Leu	
140 145 150 155	
ttt ccg cca ctt tgc ttt ctt gat ttt tcc aat ggg gaa gcc gta aag	1013
Phe Pro Pro Leu Cys Phe Leu Asp Phe Ser Asn Gly Glu Ala Val Lys	
160 165 170	

10295.204.ST25.txt

tcg cct gaa gac gaa caa acc gct gcc gga gaa gac cgc cgg gaa gaa 1061
 Ser Pro Glu Asp Glu Gln Thr Ala Ala Gly Glu Asp Arg Arg Glu Glu
 175 180 185

aaa aca gac gcg gcg gat gaa acg gta tct ggc ata gat aaa gat aaa 1109
 Lys Thr Asp Ala Ala Asp Glu Thr Val Ser Gly Ile Asp Lys Asp Lys
 190 195 200

gaa gac aaa gaa gtg aaa ttt ttt ctt gtc gaa tgg att acc ggg ctt 1157
 Glu Asp Lys Glu Val Lys Phe Phe Leu Val Glu Trp Ile Thr Gly Leu
 205 210 215

ttt tct taaaaggacc gccttgcttt cgtgtgcagg gcgggtttttt actgtttgtt 1213
 Phe Ser
 220

ttttcatgat ggttattgaa gcttttgaat atgatataat tttccaaaac gggttcagggg 1273

aaatactgct tttcggatat acaccttttg ccccttttctg atgtgccaat cacattgccg 1333

gcagaagaga aactgtctta tcaccagtac agcggttcatt tgcatactca ttcaaagcgt 1393

tggttcctgc taatcaaaat tgaaaaatga atagccggca ttcttccaaa tcaaaaggta 1453

tattttactg tcgccctcat agattggata gagaagttaa aaaacgggggt gaaaagatgt 1513

tctaccaatt gaggttagcg gaaacgaaag acatgaatgc gatcgaagca tttttaaaaa 1573

aggcgggggac aagccataag ggtcttgagg aagcgaagag ccagtttatc atgatggaag 1633

accctcccga tgaaatcgtc gcctgcctcg 1663

<210> 169

<211> 221

<212> PRT

<213> Bacillus licheniformis

<400> 169

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Gly Ala Leu Ala Asn Leu Thr Thr Glu Glu Thr Ala Gln Ser Ser Gly
 20 25 30

Gly Gln Pro Ala Val Ile Pro Asp Glu Ala Ile Arg Leu Arg Ile Leu
 35 40 45

Ala Asn Ser Asp Ser Gly Ser Asp Gln Ser Val Lys Arg Lys Ile Arg
 50 55 60

Asp Glu Val Asn Lys Gln Ile Thr Lys Trp Val Glu Asn Leu Thr Ser
 65 70 75 80

Val Glu Glu Ala Arg Gln Val Ile Arg Ser Lys Leu Pro Glu Ile Gln
 85 90 95

Glu Val Ala Met Asp Val Met Lys Arg Glu Asn Val Arg Gln Ser Val
 100 105 110

10295.204.ST25.txt

Ser Val Arg Phe Asp Arg Val Ser Phe Pro Thr Lys Leu Tyr Gly Asn
 115 120 125

Met Val Tyr Pro Ala Gly Glu Tyr Glu Ala Val Leu Ile Thr Leu Gly
 130 135 140

Lys Gly Glu Gly Ala Asn Trp Trp Cys Val Leu Phe Pro Pro Leu Cys
 145 150 155 160

Phe Leu Asp Phe Ser Asn Gly Glu Ala Val Lys Ser Pro Glu Asp Glu
 165 170 175

Gln Thr Ala Ala Gly Glu Asp Arg Arg Glu Glu Lys Thr Asp Ala Ala
 180 185 190

Asp Glu Thr Val Ser Gly Ile Asp Lys Asp Lys Glu Asp Lys Glu Val
 195 200 205

Lys Phe Phe Leu Val Glu Trp Ile Thr Gly Leu Phe Ser
 210 215 220

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<400> 170
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 aggtcaataa aggccgtgag caaaaaataa accttgtcac atcagaaccg atttcccttt 180
 tgacgaaaaa aggcgaaaat atcgaatctg ttaaaaaaga aatcaaacag aaagaagata 240
 tccaggcccc tgtcaaaaaa ggcacagagc ttgggacgct cgttttgaaa aaggatggaa 300
 aggtgctcgc tgaaagtcct cttgtcgcgtg aaaaagatat ggacaaagcg gggatgtgga 360
 cgatgttcaa gcggacgatg acccactgga cgaagtggag tgaataatgc cgaacgggtca 420
 ctagttttgt cacggtgaag gaatttataa agtctgaagc gaaacactca ttatccgatt 480
 taaaccaagg aggaatgagg atg agc ctc gga atc gat att cac gtc aaa gaa 533
 Met Ser Leu Gly Ile Asp Ile His Val Lys Glu
 1 5 10

tcc gta tta tgc att cgg ttg aca ggt gaa ctc gat cac cat aca gca 581
 Ser Val Leu Cys Ile Arg Leu Thr Gly Glu Leu Asp His His Thr Ala
 15 20 25

gaa acc ttg aga aaa caa gtc agt gac cat ctg gaa caa acc gac att 629
 Glu Thr Leu Arg Lys Gln Val Ser Asp His Leu Glu Gln Thr Asp Ile
 30 35 40

cgc cat att gtc atg aat ctt gca gac ctt tcg ttt atg gac agt tca 677

10295.204.ST25.txt

Arg His Ile Val Met Asn Leu Ala Asp Leu Ser Phe Met Asp Ser Ser
 45 50 55

ggg ctt ggc gtc gtg ctc ggc aga tat aag gag att aag cag ctc ggc 725
 Gly Leu Gly Val Val Leu Gly Arg Tyr Lys Glu Ile Lys Gln Leu Gly 75

gga gaa atg atc gtc tgc gcc att tcc cct gct gtc aaa cgt tta ttt 773
 Gly Glu Met Ile Val Cys Ala Ile Ser Pro Ala Val Lys Arg Leu Phe 90

gat atg tcc ggc ctg ttt aaa atc att cgc ctt gag caa tca gag cag 821
 Asp Met Ser Gly Leu Phe Lys Ile Ile Arg Leu Glu Gln Ser Glu Gln 105

cgt gca ctt gaa acg ttg ggc gtg gcg tca tgaaaaatga aatgaacatt 871
 Arg Ala Leu Glu Thr Leu Gly Val Ala Ser 110 115

cagttttacag cgctcagcca aaatgaatcg tttgcacggg tgacagtcgc tgctttttatc 931

gctcagcttg acccgacgat ggatgaactg accgaaatta aaacgggtcgt atccgaagcg 991

gtcacaaacg cgatcattca cggttatgaa aactcagggc agggaaacgt atatatttcc 1051

gtcactctcg aggaccatat tgtctattta acgatccgcg acgaaggagt cggcatccct 1111

aatcttgaag aagcgcgcca gccctgttc acgacaaagc ctgaactcga gcggtcggga 1171

atgggcttta cgatcatgga aaatttcatt gatgatattt cgatcgactc ctcacctgag 1231

atgggaacca caatacactt aacaaagcac ttatcaaaaa gcaaagcgct ttgcaattaa 1291

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<210> 171

<211> 117

<212> PRT

<213> Bacillus licheniformis

<400> 171

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Arg Leu Thr Gly Glu Leu Asp His His Thr Ala Glu Thr Leu Arg Lys
 20 25 30

Gln Val Ser Asp His Leu Glu Gln Thr Asp Ile Arg His Ile Val Met
 35 40 45

Asn Leu Ala Asp Leu Ser Phe Met Asp Ser Ser Gly Leu Gly Val Val
 50 55 60

Leu Gly Arg Tyr Lys Glu Ile Lys Gln Leu Gly Gly Glu Met Ile Val
 65 70 75 80

Cys Ala Ile Ser Pro Ala Val Lys Arg Leu Phe Asp Met Ser Gly Leu
 85 90 95

Phe Lys Ile Ile Arg Leu Glu Gln Ser Glu Gln Arg Ala Leu Glu Thr
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110

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10295.204.ST25.txt

125

130

135

aaa agc aaa gcg ctt tgc aat taagggagat ttgttatgga tgtggagggt 968
 Lys Ser Lys Ala Leu Cys Asn
 140 145

aaaaaagaaa accagaacac tcagcttaaa gaccatgaag tgaaagaact gattaaaaac 1028
 agccagaacg gcgatcaaaa agcaaggac ctcctcatag aaaaaaacat gcgtcttggt 1088
 tgggtctgtcg ttcagcgttt tttgaacaga ggctatgagc ctgacgacct ctttcaaadc 1148
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 <213> Bacillus licheniformis

<400> 173

Met Lys Asn Glu Met Asn Ile Gln Phe Thr Ala Leu Ser Gln Asn Glu
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 20 25 30

Thr Met Asp Glu Leu Thr Glu Ile Lys Thr Val Val Ser Glu Ala Val
 35 40 45

Thr Asn Ala Ile Ile His Gly Tyr Glu Asn Ser Gly Gln Gly Asn Val
 50 55 60

Tyr Ile Ser Val Thr Leu Glu Asp His Ile Val Tyr Leu Thr Ile Arg
 65 70 75 80

Asp Glu Gly Val Gly Ile Pro Asn Leu Glu Glu Ala Arg Gln Pro Leu
 85 90 95

Phe Thr Thr Lys Pro Glu Leu Glu Arg Ser Gly Met Gly Phe Thr Ile
 100 105 110

Met Glu Asn Phe Met Asp Asp Ile Ser Ile Asp Ser Ser Pro Glu Met
 115 120 125

Gly Thr Thr Ile His Leu Thr Lys His Leu Ser Lys Ser Lys Ala Leu
 130 135 140

Cys Asn
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<212> DNA
<213> Bacillus licheniformis
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<221> CDS
<222> (501)..(4982)
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[illegible]

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gag gga ttc ggg aag ttt gat acg tct ttg gag aac att ctt aag ccg Glu Gly Phe Gly Lys Phe Asp Thr Ser Leu Glu Asn Ile Leu Lys Pro 190 195 200	1109
agc tcc gag aca aaa aat aaa tat ccg caa tac cgc agg ccg ccg aga Ser Ser Glu Thr Lys Asn Lys Tyr Pro Gln Tyr Arg Arg Pro Pro Arg 205 210 215	1157
atg att tac gac ctg ccg gat gaa aaa gta tcc ttc agc ttc ccg gca Met Ile Tyr Asp Leu Pro Asp Glu Lys Val Ser Phe Ser Phe Pro Ala 220 225 230 235	1205
cag gaa agc gac gga gac aac aga ggc cta tgg ctg atg att ctg cct Gln Glu Ser Asp Gly Asp Asn Arg Gly Leu Trp Leu Met Ile Leu Pro 240 245 250	1253
ccg ctc gtc atg ctg atc gtc atg ggg atc gtg gcg ctc att cag ccg Pro Leu Val Met Leu Ile Val Met Gly Ile Val Ala Leu Ile Gln Pro 255 260 265	1301
cgg ggg atc ttt atc atc gtt tcc ctt gcg atg ttt atg atg acg ctg Arg Gly Ile Phe Ile Ile Val Ser Leu Ala Met Phe Met Met Thr Leu 270 275 280	1349
att acg tca acc gtg cag tac ttc cgc gac aaa aat cag cgt aaa aaa Ile Thr Ser Thr Val Gln Tyr Phe Arg Asp Lys Asn Gln Arg Lys Lys 285 290 295	1397
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aag aaa gag ctg cat gaa ctt gca gaa aga caa aag ttc gta ctt gat Lys Lys Glu Leu His Glu Leu Ala Glu Arg Gln Lys Phe Val Leu Asp 320 325 330	1493
ttc cat ttt cct aca ttt gag aga atg aaa tat tta aca aag gag atc Phe His Phe Pro Thr Phe Glu Arg Met Lys Tyr Leu Thr Lys Glu Ile 335 340 345	1541
agc gga cga att tgg gaa aaa tcg att gaa agc gcc gat ttt ctg caa Ser Gly Arg Ile Trp Glu Lys Ser Ile Glu Ser Ala Asp Phe Leu Gln 350 355 360	1589
atc cgc ctt gga acg gga aat gtt gca tct tcg tac caa atc aat ttg Ile Arg Leu Gly Thr Gly Asn Val Ala Ser Ser Tyr Gln Ile Asn Leu 365 370 375	1637
aac ggc gga gat ttg gcc aac cgc gat aca gac cat ctc ctt gaa caa Asn Gly Gly Asp Leu Ala Asn Arg Asp Thr Asp His Leu Leu Glu Gln 380 385 390 395	1685
acg caa aaa atg gaa gag gtc tac aga gag ctg aaa aat gcg ccg atc Thr Gln Lys Met Glu Glu Val Tyr Arg Glu Leu Lys Asn Ala Pro Ile 400 405 410	1733
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gtc gtc aaa aat gaa att cat cag ctt gtc ggc cag ctc gca ttt ttc Val Val Lys Asn Glu Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe 430 435 440	1829
cac agc tat cat gac ttg cgc ttt gtc ttt att ttt gac gaa gcc gag His Ser Tyr His Asp Leu Arg Phe Val Phe Ile Phe Asp Glu Ala Glu 445 450 455	1877
tat caa gaa tgg gaa tgg atg aag tgg ctc ccg cat ttt cag atg cct Tyr Gln Glu Trp Glu Trp Met Lys Trp Leu Pro His Phe Gln Met Pro 460 465 470 475	1925
cat att tat gcg aaa ggg ttt att tac aac gaa cag acg aga gat cag His Ile Tyr Ala Lys Gly Phe Ile Tyr Asn Glu Gln Thr Arg Asp Gln 480 485 490	1973
ctc ctt tca agc ata tat gag att ttg aga gaa cgg gat tta gat gaa Leu Leu Ser Ser Ile Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu 495 500 505	2021
aac aaa aag aag act ttg ttt aag ccg cac ttt gtg ttt atc atc aca Asn Lys Lys Lys Thr Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr 510 515 520	2069
aat cag cag ctc atc gca gaa cac gtc att tta gaa tat ttg gaa ggc Asn Gln Gln Leu Ile Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly 525 530 535	2117
aag cag aaa cac ctc gga gtg tcg aca atc gtg gcg gca gag aca aaa Lys Gln Lys His Leu Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys 540 545 550 555	2165
gaa agc ctg tcc gaa aac att cat acc ctt gtt cgt tat att act gaa Glu Ser Leu Ser Glu Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu 560 565 570	2213
cag gaa ggc gac att ctg atc aag caa aag aaa gcc gtc cag atc ccg Gln Glu Gly Asp Ile Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro 575 580 585	2261
ttt cag ctg gat cac cac aac agg gaa gac aac gaa cag ttt tcc ccg Phe Gln Leu Asp His His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg 590 595 600	2309
acg ctg aga acg ctt gac cac cag acg ggc atg acg aat tcg att cct Thr Leu Arg Thr Leu Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro 605 610 615	2357
gat acc gta tcg ttt ctc gaa ctg ttc caa gtg aag gaa gtc gat gac Asp Thr Val Ser Phe Leu Glu Leu Phe Gln Val Lys Glu Val Asp Asp 620 625 630 635	2405
atc ggc atc gaa caa aaa tgg atg aca agc gaa tcg gcc aaa tct ttg Ile Gly Ile Glu Gln Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu 640 645 650	2453
gcc gtg ccg atc ggc tat aaa gga aaa gac gac att gtt tat tta aac Ala Val Pro Ile Gly Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn 655 660 665	2501
ctt cac gaa aag gcg cac ggc ccc cac ggg ctg ctt gcc gga acg acc Leu His Glu Lys Ala His Gly Pro His Gly Leu Leu Ala Gly Thr Thr 670 675 680	2549
ggt tcg ggt aaa agt gaa ttt ttg cag act tat att ttg tct ttg gca Gly Ser Gly Lys Ser Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala 685 690 695	2597

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gtt cac ttt cac ccg cat gaa gtc gca ttt ttg cta atc gac tac aaa 2645
 Val His Phe His Pro His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys
 700 705 710 715
 ggg ggc gga atg gcg cag ccg ttc cgg aac att ccg cat ttg ctc gga 2693
 Gly Gly Gly Met Ala Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly
 720 725 730
 acg att act aac att gaa ggc agc aag aac ttc agc aac cgg gcg ctt 2741
 Thr Ile Thr Asn Ile Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu
 735 740 745
 gcg tcc att aag agc gag ctg aag aaa agg cag ccg ctc ttt gat cag 2789
 Ala Ser Ile Lys Ser Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln
 750 755 760
 tac aaa gtg aac cat atc aac gac tat aca aag ctt tac aaa cag aaa 2837
 Tyr Lys Val Asn His Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys
 765 770 775
 aaa gcg aaa acg gcg atg ccg cac ctt ttc tta att tca gac gaa ttt 2885
 Lys Ala Lys Thr Ala Met Pro His Leu Phe Leu Ile Ser Asp Glu Phe
 780 785 790 795
 gcc gag ctg aaa agc gaa gaa ccg gaa ttt atc cgc gag ctt gtc agt 2933
 Ala Glu Leu Lys Ser Glu Glu Pro Glu Phe Ile Arg Glu Leu Val Ser
 800 805 810
 gcg gca agg atc ggg cga agc ctc ggg gtg cac tta atc ttg gcg acg 2981
 Ala Ala Arg Ile Gly Arg Ser Leu Gly Val His Leu Ile Leu Ala Thr
 815 820 825
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 Gln Lys Pro Gly Gly Ile Ile Asp Asp Gln Ile Trp Ser Asn Ser Arg
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 Phe Lys Val Ala Leu Lys Val Gln Asp Ala Asn Asp Ser Lys Glu Ile
 845 850 855
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 Leu Lys Asn Gly Asp Ala Ala Thr Ile Thr Val Thr Gly Arg Gly Tyr
 860 865 870 875
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 880 885 890
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 Ser Gly Ala Pro Tyr Met Glu Asp Gly Tyr Gly Thr Glu Asp Glu Val
 895 900 905
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 Ala Ile Val Thr Asp Thr Gly Leu Ile Pro Leu Ser Asp Val Asp Ala
 910 915 920
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 Asp Arg Ala Ala Lys Lys Glu Ala Val Thr Glu Ile Ser Ala Val Val
 925 930 935
 gaa caa att gaa cgg att caa gcg gag atg gga atc gag aag ctc ccg 3365
 Glu Gln Ile Glu Arg Ile Gln Ala Glu Met Gly Ile Glu Lys Leu Pro
 940 945 950 955
 agc cct tgg ctg ccg ccg ctt gaa gaa cgc ata ccg aaa acg cgc tat 3413
 Ser Pro Trp Leu Pro Pro Leu Glu Glu Arg Ile Pro Lys Thr Arg Tyr
 960 965 970

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ccg tcg gag gaa gcc gat gcc ttt aac ttt gcc tat atc gat gaa cct Pro Ser Glu Glu Ala Asp Ala Phe Asn Phe Ala Tyr Ile Asp Glu Pro 975 980 985	3461
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aat atc ggc atc gtc ggc tcg tca ggc tac gga aaa tcc ctg aca Asn Ile Gly Ile Val Gly Ser Ser Gly Tyr Gly Lys Ser Leu Thr 1005 1010 1015	3554
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gaa ttg cat tac tac att ttc gac ttt ggc aac gga acg ctg ctt Glu Leu His Tyr Tyr Ile Phe Asp Phe Gly Asn Gly Thr Leu Leu 1035 1040 1045	3644
ccg ctt gca agg ctt ccg cac acc gcg gat tat ttc ctg atg gac Pro Leu Ala Arg Leu Pro His Thr Ala Asp Tyr Phe Leu Met Asp 1050 1055 1060	3689
caa acg aga aaa atc gag aaa ttt atg gtc cgg atc aag gcg gaa Gln Thr Arg Lys Ile Glu Lys Phe Met Val Arg Ile Lys Ala Glu 1065 1070 1075	3734
atc gag cac agg aaa aat ctc ttc cgt gca aaa gaa atc agc cat Ile Glu His Arg Lys Asn Leu Phe Arg Ala Lys Glu Ile Ser His 1080 1085 1090	3779
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gat atc gag ctg ttt gaa ggg atc aaa gcc gac att cag gcg atc Asp Ile Glu Leu Phe Glu Gly Ile Lys Ala Asp Ile Gln Ala Ile 1215 1220 1225	4184

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act gtc gaa ccc gta tac ttt aat ctt gag aaa aat aag cac tgc Thr Val Glu Pro Val Tyr Phe Asn Leu Glu Lys Asn Lys His Cys 1275 1280 1285	4364
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gtg ttt gat tcg ata gac aga ggg ctt tct caa tat gcg aca gag Val Phe Asp Ser Ile Asp Arg Gly Leu Ser Gln Tyr Ala Thr Glu 1320 1325 1330	4499
gat caa atc agc tat cta gaa aca aaa gac gac att ctg ctc tgg Asp Gln Ile Ser Tyr Leu Glu Thr Lys Asp Asp Ile Leu Leu Trp 1335 1340 1345	4544
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gag ttc aca aaa ggc tat gat tcg ctg aca agc gaa gtc aag cag Glu Phe Thr Lys Gly Tyr Asp Ser Leu Thr Ser Glu Val Lys Gln 1425 1430 1435	4814
gtc aga cac gcg atg cta ttg atg aaa aaa tcc gag cag aac ttg Val Arg His Ala Met Leu Leu Met Lys Lys Ser Glu Gln Asn Leu 1440 1445 1450	4859
att cag ctc cca tat gaa cgc cag gag ccg gaa att ctg ccg ggc Ile Gln Leu Pro Tyr Glu Arg Gln Glu Pro Glu Ile Leu Pro Gly 1455 1460 1465	4904
ttt ggc tat atc gtt gaa aac ggc aaa gag agg aaa att caa att Phe Gly Tyr Ile Val Glu Asn Gly Lys Glu Arg Lys Ile Gln Ile 1470 1475 1480	4949

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 1485 1490

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<210> 175
 <211> 1494
 <212> PRT
 <213> Bacillus licheniformis

<400> 175

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 20 25 30

His Ser Val Thr Ile Lys His Phe Ser Phe Glu Lys Gly Pro Val Thr
 35 40 45

Leu Glu Lys Gln Lys Asp Ser Asp Ala Leu Asn Val Gln Leu Gly Gly
 50 55 60

Glu Thr Val Ser Ser Leu Lys Leu Gly Gly Lys Ala Ser Val Gln Ser
 65 70 75 80

Gly Ala Glu Gln Leu Thr Leu Phe Leu Ala Glu Glu Ala Asp Ser Val
 85 90 95

Pro Ala Tyr Tyr Leu Gly Glu Arg Gln Glu Ile Val Ile Ser Ser Leu
 100 105 110

Asp Gln Glu Ala Asp Val Tyr Phe Asn Glu Thr Asp Ser Phe Phe Gly
 115 120 125

Glu Lys Gly Thr Phe Ser Phe Ile Arg Leu Asp Gly Gln Trp Asn Val
 130 135 140

Leu Pro Asn Asp Ala Lys Ile Tyr Leu Asn Gly Glu Glu Val Ser Ala
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145

150

155

160

Pro Val Ser Val Gln Asn Gly Asp Glu Ile Ala Phe Gly Leu Asn Ile
 165 170 175

Leu Arg Ile Val Glu Asp Asp Leu Leu Glu Ile Glu Gly Phe Gly Lys
 180 185 190

Phe Asp Thr Ser Leu Glu Asn Ile Leu Lys Pro Ser Ser Glu Thr Lys
 195 200 205

Asn Lys Tyr Pro Gln Tyr Arg Arg Pro Pro Arg Met Ile Tyr Asp Leu
 210 215 220

Pro Asp Glu Lys Val Ser Phe Ser Phe Pro Ala Gln Glu Ser Asp Gly
 225 230 235 240

Asp Asn Arg Gly Leu Trp Leu Met Ile Leu Pro Pro Leu Val Met Leu
 245 250 255

Ile Val Met Gly Ile Val Ala Leu Ile Gln Pro Arg Gly Ile Phe Ile
 260 265 270

Ile Val Ser Leu Ala Met Phe Met Met Thr Leu Ile Thr Ser Thr Val
 275 280 285

Gln Tyr Phe Arg Asp Lys Asn Gln Arg Lys Lys Arg Glu Glu Lys Arg
 290 295 300

Glu Arg Val Tyr Thr Leu Tyr Leu Glu Asn Lys Lys Lys Glu Leu His
 305 310 315 320

Glu Leu Ala Glu Arg Gln Lys Phe Val Leu Asp Phe His Phe Pro Thr
 325 330 335

Phe Glu Arg Met Lys Tyr Leu Thr Lys Glu Ile Ser Gly Arg Ile Trp
 340 345 350

Glu Lys Ser Ile Glu Ser Ala Asp Phe Leu Gln Ile Arg Leu Gly Thr
 355 360 365

Gly Asn Val Ala Ser Ser Tyr Gln Ile Asn Leu Asn Gly Gly Asp Leu
 370 375 380

Ala Asn Arg Asp Thr Asp His Leu Leu Glu Gln Thr Gln Lys Met Glu
 385 390 395 400

Glu Val Tyr Arg Glu Leu Lys Asn Ala Pro Ile Thr Val Asn Leu Ala
 405 410 415

Glu Gly Pro Met Gly Val Val Gly Lys Leu Ser Val Val Lys Asn Glu
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420

425

430

Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe His Ser Tyr His Asp
 435 440 445

Leu Arg Phe Val Phe Ile Phe Asp Glu Ala Glu Tyr Gln Glu Trp Glu
 450 455 460

Trp Met Lys Trp Leu Pro His Phe Gln Met Pro His Ile Tyr Ala Lys
 465 470 475 480

Gly Phe Ile Tyr Asn Glu Gln Thr Arg Asp Gln Leu Leu Ser Ser Ile
 485 490 495

Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu Asn Lys Lys Lys Thr
 500 505 510

Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr Asn Gln Gln Leu Ile
 515 520 525

Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly Lys Gln Lys His Leu
 530 535 540

Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys Glu Ser Leu Ser Glu
 545 550 555 560

Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu Gln Glu Gly Asp Ile
 565 570 575

Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro Phe Gln Leu Asp His
 580 585 590

His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg Thr Leu Arg Thr Leu
 595 600 605

Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro Asp Thr Val Ser Phe
 610 615 620

Leu Glu Leu Phe Gln Val Lys Glu Val Asp Asp Ile Gly Ile Glu Gln
 625 630 635 640

Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu Ala Val Pro Ile Gly
 645 650 655

Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn Leu His Glu Lys Ala
 660 665 670

His Gly Pro His Gly Leu Leu Ala Gly Thr Thr Gly Ser Gly Lys Ser
 675 680 685

Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala Val His Phe His Pro
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700

690

695

His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys Gly Gly Gly Met Ala
705 710 715 720

Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly Thr Ile Thr Asn Ile
725 730 735

Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu Ala Ser Ile Lys Ser
740 745 750

Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln Tyr Lys Val Asn His
755 760 765

Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys Lys Ala Lys Thr Ala
770 775 780

Met Pro His Leu Phe Leu Ile Ser Asp Glu Phe Ala Glu Leu Lys Ser
785 790 795 800

Glu Glu Pro Glu Phe Ile Arg Glu Leu Val Ser Ala Ala Arg Ile Gly
805 810 815

Arg Ser Leu Gly Val His Leu Ile Leu Ala Thr Gln Lys Pro Gly Gly
820 825 830

Ile Ile Asp Asp Gln Ile Trp Ser Asn Ser Arg Phe Lys Val Ala Leu
835 840 845

Lys Val Gln Asp Ala Asn Asp Ser Lys Glu Ile Leu Lys Asn Gly Asp
850 855 860

Ala Ala Thr Ile Thr Val Thr Gly Arg Gly Tyr Leu Gln Val Gly Asn
865 870 875 880

Asn Glu Val Tyr Glu Leu Phe Gln Ser Ala Trp Ser Gly Ala Pro Tyr
885 890 895

Met Glu Asp Gly Tyr Gly Thr Glu Asp Glu Val Ala Ile Val Thr Asp
900 905 910

Thr Gly Leu Ile Pro Leu Ser Asp Val Asp Ala Asp Arg Ala Ala Lys
915 920 925

Lys Glu Ala Val Thr Glu Ile Ser Ala Val Val Glu Gln Ile Glu Arg
930 935 940

Ile Gln Ala Glu Met Gly Ile Glu Lys Leu Pro Ser Pro Trp Leu Pro
945 950 955 960

Pro Leu Glu Glu Arg Ile Pro Lys Thr Arg Tyr Pro Ser Glu Glu Ala
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965

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970

975

Asp Ala Phe Asn Phe Ala Tyr Ile Asp Glu Pro Glu Lys Gln Ser Gln
 980 985 990

Glu Pro Ile Ser Tyr Arg Met Met Glu Asp Gly Asn Ile Gly Ile Val
 995 1000 1005

Gly Ser Ser Gly Tyr Gly Lys Ser Leu Thr Ala Thr Thr Phe Met
 1010 1015 1020

Met Ser Phe Ala Glu Gln Tyr Thr Pro Glu Glu Leu His Tyr Tyr
 1025 1030 1035

Ile Phe Asp Phe Gly Asn Gly Thr Leu Leu Pro Leu Ala Arg Leu
 1040 1045 1050

Pro His Thr Ala Asp Tyr Phe Leu Met Asp Gln Thr Arg Lys Ile
 1055 1060 1065

Glu Lys Phe Met Val Arg Ile Lys Ala Glu Ile Glu His Arg Lys
 1070 1075 1080

Asn Leu Phe Arg Ala Lys Glu Ile Ser His Ile Lys Met Tyr Asn
 1085 1090 1095

Ala Leu Asn Glu Glu Lys Leu Pro Phe Ile Phe Ile Thr Val Asp
 1100 1105 1110

Asn Phe Asp Ile Ile Lys Asp Glu Met His Glu Leu Glu Ser Glu
 1115 1120 1125

Phe Ile Gln Phe Ser Arg Asp Gly Gln Ser Leu Gly Ile Tyr Leu
 1130 1135 1140

Ile Leu Thr Ala Thr Arg Val Asn Ala Ile Arg Gln Ser Leu Leu
 1145 1150 1155

Asn Asn Leu Lys Thr Arg Val Val His Tyr Leu Met Asp Gln Ser
 1160 1165 1170

Glu Ala Tyr Ser Ile Ile Gly Arg Pro Glu Phe Ser Leu Glu Pro
 1175 1180 1185

Ile Pro Gly Arg Val Ile Ile Asn Lys Glu Asn Gln Tyr Phe Ala
 1190 1195 1200

Gln Met Phe Met Pro Val Glu Ala Asp Asn Asp Ile Glu Leu Phe
 1205 1210 1215

Glu Gly Ile Lys Ala Asp Ile Gln Ala Ile Ala Glu Arg Ser Glu
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1220

1225

1230

Gly Met Arg Lys Pro Ala Pro Val Pro Met Leu Pro Leu Glu Leu
 1235 1240 1245
 Ser Val Thr Gln Phe Val Arg Asp Tyr Pro Leu Gln Pro Glu Arg
 1250 1255 1260
 Gly Leu Ile Pro Met Gly Leu Asp Glu Glu Thr Val Glu Pro Val
 1265 1270 1275
 Tyr Phe Asn Leu Glu Lys Asn Lys His Cys Leu Ile Met Gly Gln
 1280 1285 1290
 Thr Gln Arg Gly Lys Thr Asn Val Ile Lys Ile Met Leu Glu His
 1295 1300 1305
 Leu Leu Asp His Asp Thr Lys Lys Ile Ala Val Phe Asp Ser Ile
 1310 1315 1320
 Asp Arg Gly Leu Ser Gln Tyr Ala Thr Glu Asp Gln Ile Ser Tyr
 1325 1330 1335
 Leu Glu Thr Lys Asp Asp Ile Leu Leu Trp Leu Ala Glu Thr Glu
 1340 1345 1350
 Glu Ile Cys Arg Thr Arg Glu Ala Met Tyr Leu Glu Ala Val Lys
 1355 1360 1365
 Gln Gly Glu Ile Ala Asn Leu Asp Phe Ser Pro Met Val Phe Ile
 1370 1375 1380
 Val Asp Gly Ile Ser Arg Phe Gln Gln Thr Ile Asp Ala Ser Ile
 1385 1390 1395
 Gln Asp Lys Met Ala Met Phe Met Lys Ser Tyr Ala His Leu Gly
 1400 1405 1410
 Phe His Phe Ile Pro Ala Gly Asn His Ser Glu Phe Thr Lys Gly
 1415 1420 1425
 Tyr Asp Ser Leu Thr Ser Glu Val Lys Gln Val Arg His Ala Met
 1430 1435 1440
 Leu Leu Met Lys Lys Ser Glu Gln Asn Leu Ile Gln Leu Pro Tyr
 1445 1450 1455
 Glu Arg Gln Glu Pro Glu Ile Leu Pro Gly Phe Gly Tyr Ile Val
 1460 1465 1470
 Glu Asn Gly Lys Glu Arg Lys Ile Gln Ile Pro Leu Cys Ala Val
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1480

1485

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125	130	135	
cct gat ctt gga ggc gga atg att gga gcc ctt tta ttc gcg gcg tca Pro Asp Leu Gly Gly Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser 140 145 150 155			965
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atc ttg atc ggc ctt ctt ttg att acg gat cgg tcg ctt cag gag acg Ile Leu Ile Gly Leu Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr 175 180 185			1061
ctg atc aaa tgg atg acc ccg gtc gcc tcc ttc atg aaa aac cag tgg Leu Ile Lys Trp Met Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp 190 195 200			1109
cag gcc ttt tta gca gat ctt aaa caa ttg aaa aac agc tcg ccg aaa Gln Ala Phe Leu Ala Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys 205 210 215			1157
aag aaa tcc gga aaa aaa caa aag acg cag aga aaa ccg aaa gtg tct Lys Lys Ser Gly Lys Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser 220 225 230 235			1205
gaa gag cct gta caa gaa gcg gac ctt gat cca gat ccg gtt att caa Glu Glu Pro Val Gln Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln 240 245 250			1253
tca gaa ccg att att tca agc ttt tcc gac cgt gat gaa aag ccc gaa Ser Glu Pro Ile Ile Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu 255 260 265			1301
gtt caa gct tac gaa gct ccg gcg gct cct gct gaa cct cct gct gag Val Gln Ala Tyr Glu Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu 270 275 280			1349
ccc gaa atc ggt gag gaa atg cag gcc tcc ggc gcg ccc gaa atc acg Pro Glu Ile Gly Glu Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr 285 290 295			1397
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tac gac aat gcc agg aag ctg gaa agg acg ttt caa agc ttc gga gtt Tyr Asp Asn Ala Arg Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val 335 340 345			1541
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gcc ccg atc ccc gga aaa tcg gcg att gga atc gaa gtg ccg aat gcg Ala Pro Ile Pro Gly Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala 1733			

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Glu	Val	Ala	Met	Val	Ser	Leu	Lys	Glu	Val	Leu	Glu	Ser	Lys	Leu	Asn															
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460				465					470					475																
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Lys	Lys	Val	Val	Asn	Glu	Met	Glu	Arg	Arg	Tyr	Glu	Leu	Phe	Ser	His															
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Thr	Gly	Thr	Arg	Asn	Ile	Glu	Gly	Tyr	Asn	Asp	Tyr	Ile	Lys	Arg	Met															
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Glu	Asp	Ser	Ile	Thr	Arg	Leu	Ser	Gln	Met	Ala	Arg	Ala	Ala	Gly	Ile															
		590					595					600																		
cac	ctg	atc	att	gcg	acg	cag	agg	cct	tcg	gtc	gat	gtt	atc	aca	ggg		2357													
His	Leu	Ile	Ile	Ala	Thr	Gln	Arg	Pro	Ser	Val	Asp	Val	Ile	Thr	Gly															
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Val	Ile	Lys	Ala	Asn	Ile	Pro	Ser	Arg	Ile	Ala	Phe	Ser	Val	Ser	Ser															
620					625					630					635															
cag	acc	gac	tcc	agg	acg	att	ctt	gat	atg	gga	ggc	gct	gaa	aaa	ctt		2453													
Gln	Thr	Asp	Ser	Arg	Thr	Ile	Leu	Asp	Met	Gly	Gly	Ala	Glu	Lys	Leu															
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ctc	ggc	aga	ggg	gac	atg	ctg	ttt	ctc	cct	gtc	ggc	gcc	aat	aaa	ccg		2501													
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Leu	Arg	Val	Gln	Gly	Ala	Phe	Leu	Ser	Asp	Glu	Glu	Val	Glu	Lys	Val															

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670 675 680

gtc gat cac gtc atc agc cag caa aaa gcc caa tac caa gaa gaa atg 2597
Val Asp His Val Ile Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met
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Ile Pro Glu Glu Thr Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu
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Tyr Asp Glu Ala Val Ala Leu Val Val Ser Met Gln Thr Ala Ser Val
720 725 730

tcc atg ctg caa agg aga ttc cgc atc ggc tat aca aga gcg gcg cgg 2741
Ser Met Leu Gln Arg Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg
735 740 745

ctt atc gat gcc atg gaa gag cgg gga atc gtc ggc cca tat gaa gga 2789
Leu Ile Asp Ala Met Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly
750 755 760

tca aaa ccc cgt gaa gtt ctc ttg tca aaa gag caa tac gaa gaa ctc 2837
Ser Lys Pro Arg Glu Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu
765 770 775

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Ser Ser
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<213> Bacillus licheniformis

<400> 177

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20 25 30

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35 40 45

Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp Phe Ile Leu Cys Leu
50 55 60

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Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe Trp Lys Lys Lys Thr
 65 70 75 80
 Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu Tyr Cys Ile Ile Ala
 85 90 95
 Ser Met Leu Leu Leu Ser His Val Gln Leu Phe Gln His Leu Thr Glu
 100 105 110
 Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln Asn Thr Trp Glu Leu
 115 120 125
 Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser Pro Asp Leu Gly Gly
 130 135 140
 Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser Tyr Phe Leu Phe Ala
 145 150 155 160
 Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu Ile Leu Ile Gly Leu
 165 170 175
 Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr Leu Ile Lys Trp Met
 180 185 190
 Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp Gln Ala Phe Leu Ala
 195 200 205
 Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys Lys Lys Ser Gly Lys
 210 215 220
 Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser Glu Glu Pro Val Gln
 225 230 235 240
 Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln Ser Glu Pro Ile Ile
 245 250 255
 Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu Val Gln Ala Tyr Glu
 260 265 270
 Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu Pro Glu Ile Gly Glu
 275 280 285
 Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr Phe Thr Glu Leu Glu
 290 295 300
 Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu Leu Asp Asp Pro Lys
 305 310 315 320
 His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile Tyr Asp Asn Ala Arg
 325 330 335
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Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val Lys Ala Lys Val Thr
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 Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr Glu Val Tyr Pro Asp
 355 360 365
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 370 375 380
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 385 390 395 400
 Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala Glu Val Ala Met Val
 405 410 415
 Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn Asp Arg Pro Asp Ala
 420 425 430
 Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser Gly Glu Ala Val Leu
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 Ala Glu Leu Asn Lys Met Pro His Leu Leu Val Ala Gly Ala Thr Gly
 450 455 460
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 465 470 475 480
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 485 490 495
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 500 505 510
 Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu Lys Lys Val Val Asn
 515 520 525
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 545 550 555 560
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 580 585 590
 Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile His Leu Ile Ile Ala
 595 600 605

10295.204.ST25.txt

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675 680 685

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690 695 700

Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu Tyr Asp Glu Ala Val
705 710 715 720

Ala Leu Val Val Ser Met Gln Thr Ala Ser Val Ser Met Leu Gln Arg
725 730 735

Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg Leu Ile Asp Ala Met
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755 760 765

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10295.204.ST25.txt

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ataaaaaaag cggaataa gaccgttttc ctgcccaagc atcaggcata cgctaataaa 480
aaaggaaaag ggtgtatcct atg ata agt gtt tgc ggc tac cgg ctc cgt cct 533
Met Ile Ser Val Ser Gly Tyr Arg Leu Arg Pro
1 5 10
gag gat atc gaa aaa ctg aat gtc agt cag acg cag aga gac atc gca 581
Glu Asp Ile Glu Lys Leu Asn Val Ser Gln Thr Gln Arg Asp Ile Ala
15 20 25
aac cgg atg ctg gcc atg ccg tcc gga tat aga tac ggt tca atc tca 629
Asn Arg Met Leu Ala Met Pro Ser Gly Tyr Arg Tyr Gly Ser Ile Ser
30 35 40
gaa ctg tta ttt gag ctg aga ttc aga gag cat acc gtc aaa tgc gcc 677
Glu Leu Leu Phe Glu Leu Arg Phe Arg Glu His Thr Val Lys Ser Ala
45 50 55
aga gag ctg atc aac agc gga gcg aag ttt gcc acc ttt tca aag aca 725
Arg Glu Leu Ile Asn Ser Gly Ala Lys Phe Ala Thr Phe Ser Lys Thr
60 65 70 75
tac ggg aat gaa gag ttt tgg agg gtg acg cct gag ggg gct ttg gag 773
Tyr Gly Asn Glu Glu Phe Trp Arg Val Thr Pro Glu Gly Ala Leu Glu
80 85 90
ttg aag tac agg gca ccg gct tca aag gcg att cga aat att ttt gaa 821
Leu Lys Tyr Arg Ala Pro Ala Ser Lys Ala Ile Arg Asn Ile Phe Glu
95 100 105
agc ggc cct tct tat gct ttt gag tgc gcg act gcg att gtc atc att 869
Ser Gly Pro Ser Tyr Ala Phe Glu Cys Ala Thr Ala Ile Val Ile Ile
110 115 120
ttt tat atg gcg ctt ctc aaa acg atc ggc gac cag aca ttt gac cgg 917
Phe Tyr Met Ala Leu Leu Lys Thr Ile Gly Asp Gln Thr Phe Asp Arg
125 130 135
aat tat caa agg atc att tta tac gat tgg cac tat gag cgg ctg ccg 965
Asn Tyr Gln Arg Ile Ile Leu Tyr Asp Trp His Tyr Glu Arg Leu Pro
140 145 150 155
atc tat acg gat aaa gga aac gac tac ctt ccg gga gac tgc ctg tat 1013
Ile Tyr Thr Asp Lys Gly Asn Asp Tyr Leu Pro Gly Asp Cys Leu Tyr
160 165 170
ttc aag aac cct gaa ttc gat ccc tca aga ccg cag tgg cgc gga gaa 1061
Phe Lys Asn Pro Glu Phe Asp Pro Ser Arg Pro Gln Trp Arg Gly Glu
175 180 185
aat gct att tta ctt gaa aat aat ctc tat gcg gca cac ggc ctg ggg 1109
Asn Ala Ile Leu Leu Glu Asn Asn Leu Tyr Ala Ala His Gly Leu Gly
190 195 200
atc tta agc ggc gaa aca atc att gaa aaa ctg aac ggg ctg aga aag 1157
Ile Leu Ser Gly Glu Thr Ile Ile Glu Lys Leu Asn Gly Leu Arg Lys
205 210 215
cct cat gca cag acg tcc gcc tat ctg ctt tcc caa gtg acg cgg gtt 1205
Pro His Ala Gln Thr Ser Ala Tyr Leu Leu Ser Gln Val Thr Arg Val
220 225 230 235
gat att ccg gca tta att caa atg atc aga tagcacatcg gccggcaca 1255
Asp Ile Pro Ala Leu Ile Gln Met Ile Arg
240 245

10295.204.ST25.txt

gctgatccat cagctccttc accgtcgttt gctcgacggt ggcccgcacg ctctgtccgg 1315
 cccacaatga catgttatcc gtattcccgt caagcttcgc ctgttttctc atcggttgcg 1375
 tcagcgtggt ttgcagagga taaggcagcg cttcagcttc ttcctggcgt ctgtcttcca 1435
 tccactgatt gacgatgcct cttgccggct tccccgagaa caaacgggtc aggcttggtg 1495
 cggtttcaac cgcttcgaac aatttttggt tgtaggcagg gtgtgttcg ctttcttcgc 1555
 acgtcaaaaa agcgggtaccg atttgaacgc cctgtgcgcc gagggcaaaa gctgcagcaa 1615
 cacctctttt gtcaaaaatg ccgcccgtg cgataactgg aaccgacaca tgatctgccg 1675
 cttggggaat taaagccatc gagccgacag caggctctcc cttcgttttc aagaaggctc 1735

<210> 179
 <211> 245
 <212> PRT
 <213> Bacillus licheniformis

<400> 179

Met Ile Ser Val Ser Gly Tyr Arg Leu Arg Pro Glu Asp Ile Glu Lys
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 20 25 30

Met Pro Ser Gly Tyr Arg Tyr Gly Ser Ile Ser Glu Leu Leu Phe Glu
 35 40 45

Leu Arg Phe Arg Glu His Thr Val Lys Ser Ala Arg Glu Leu Ile Asn
 50 55 60

Ser Gly Ala Lys Phe Ala Thr Phe Ser Lys Thr Tyr Gly Asn Glu Glu
 65 70 75 80

Phe Trp Arg Val Thr Pro Glu Gly Ala Leu Glu Leu Lys Tyr Arg Ala
 85 90 95

Pro Ala Ser Lys Ala Ile Arg Asn Ile Phe Glu Ser Gly Pro Ser Tyr
 100 105 110

Ala Phe Glu Cys Ala Thr Ala Ile Val Ile Ile Phe Tyr Met Ala Leu
 115 120 125

Leu Lys Thr Ile Gly Asp Gln Thr Phe Asp Arg Asn Tyr Gln Arg Ile
 130 135 140

Ile Leu Tyr Asp Trp His Tyr Glu Arg Leu Pro Ile Tyr Thr Asp Lys
 145 150 155 160

Gly Asn Asp Tyr Leu Pro Gly Asp Cys Leu Tyr Phe Lys Asn Pro Glu
 165 170 175

10295.204.ST25.txt

Phe Asp Pro Ser Arg Pro Gln Trp Arg Gly Glu Asn Ala Ile Leu Leu
 180 185 190

Glu Asn Asn Leu Tyr Ala Ala His Gly Leu Gly Ile Leu Ser Gly Glu
 195 200 205

Thr Ile Ile Glu Lys Leu Asn Gly Leu Arg Lys Pro His Ala Gln Thr
 210 215 220

Ser Ala Tyr Leu Leu Ser Gln Val Thr Arg Val Asp Ile Pro Ala Leu
 225 230 235 240

Ile Gln Met Ile Arg
 245

<210> 180
 <211> 1405
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(905)

<400> 180
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 cacatactca ctgaggcgga acgccaaaac aacaaaaaac ggaaaaccaa tcaataaata 180
 cgaaagatcc ttcatgaata tcttaggagg ttaaaacatt gacaaataaa aacgacggca 240
 aagatatgcg caaaaacgca ccgaaaggag ctgagccggg gcagccagag cctttgagcg 300
 gaagcaaaaa agtaaaaaac cggaaccata caagacaaaa acacaattcc agtcacgata 360
 tgtaacattt tttccgcgcc tttcacggcg cggttttttt ccttaccgcg cgtcaccctg 420
 aggcgttggtc caccctcctt cacatgaatt caaagggtgtg cataatctaa tggtaggct 480
 aggtatggag gaatgctcca atg aca aat aca aaa cgt ttc gat tcc gca gat 533
 Met Thr Asn Thr Lys Arg Phe Asp Ser Ala Asp
 1 5 10
 ttt gat aaa gaa tgg atg aaa cag ttt gtt gac gac cct ttt ctc ctc 581
 Phe Asp Lys Glu Trp Met Lys Gln Phe Val Asp Asp Pro Phe Leu Leu
 15 20 25
 tat gat gaa act tta ccg att gac ctt tat gaa acg agc act gaa tat 629
 Tyr Asp Glu Thr Leu Pro Ile Asp Leu Tyr Glu Thr Ser Thr Glu Tyr
 30 35 40
 ata att gaa gca gat tta agc cac ttg aat gtc cgg cat ctt gac ttg 677
 Ile Ile Glu Ala Asp Leu Ser His Leu Asn Val Arg His Leu Asp Leu
 45 50 55
 acg ttt tca ggc tac gat ttc aag ctt gca gtt aaa acc gat gag cag 725
 Thr Phe Ser Gly Tyr Asp Phe Lys Leu Ala Val Lys Thr Asp Glu Gln
 60 65 70 75

10295.204.ST25.txt

ctt tac gag aaa tcg ctg atg ctt cct ttc ttt ttg aat gac aaa cag 773
 Leu Tyr Glu Lys Ser Leu Met Leu Pro Phe Phe Leu Asn Asp Lys Gln
 80 85 90
 atc gaa gcg gaa tgc gaa aac aac att ctt gca gtt aaa atc aat aaa 821
 Ile Glu Ala Glu Cys Glu Asn Asn Ile Leu Ala Val Lys Ile Asn Lys
 95 100 105
 gaa tca agc aaa gat gac att tcg ctt tca atc aat att cct ttt ata 869
 Glu Ser Ser Lys Asp Asp Ile Ser Leu Ser Ile Asn Ile Pro Phe Ile
 110 115 120
 tca aac ctg cac aac aag cag aac ccg gac agc gct taaaacactt 915
 Ser Asn Leu His Asn Lys Gln Asn Pro Asp Ser Ala
 125 130 135
 gccatccggg tttttttccg ttcgttcgtc aaatatcctc tagcaattct ctatggccga 975
 ttagggaatc gctatacaat agattatgtt ctagcatctc ttttgaccag gccggtgtcc 1035
 cattttatat ttttttttct atgttcttct aaaacgcctt catgtaaaat aggttataga 1095
 caaaggagtg atgagagatg ctggaaggat ggtttttatg gctgatgctc gcttggatcg 1155
 tcatcatgat cgtcctcttg tcaatcggcg gttttttcat gtttcgcaaa tttttaaaaa 1215
 ggctgcctaa agaagatggg aaatctgagc tggactggca ggattattat attgaacaga 1275
 caaggcattt gtggaatgac gaagaaaaag aactgcttga ggaattgggt tcaccggtac 1335
 ccgagctggt tcgcatgta gcaaaagcaa aaatcgccgg taagatcggg gagcttgcac 1395
 tgaaagaaaa 1405

<210> 181
 <211> 135
 <212> PRT
 <213> Bacillus licheniformis
 <400> 181

Met Thr Asn Thr Lys Arg Phe Asp Ser Ala Asp Phe Asp Lys Glu Trp
 1 5 10 15

Met Lys Gln Phe Val Asp Asp Pro Phe Leu Leu Tyr Asp Glu Thr Leu
 20 25 30

Pro Ile Asp Leu Tyr Glu Thr Ser Thr Glu Tyr Ile Ile Glu Ala Asp
 35 40 45

Leu Ser His Leu Asn Val Arg His Leu Asp Leu Thr Phe Ser Gly Tyr
 50 55 60

Asp Phe Lys Leu Ala Val Lys Thr Asp Glu Gln Leu Tyr Glu Lys Ser
 65 70 75 80

Leu Met Leu Pro Phe Phe Leu Asn Asp Lys Gln Ile Glu Ala Glu Cys
 85 90 95

Glu Asn Asn Ile Leu Ala Val Lys Ile Asn Lys Glu Ser Ser Lys Asp
 100 105 110

Asp Ile Ser Leu Ser Ile Asn Ile Pro Phe Ile Ser Asn Leu His Asn
115 120 125

Lys Gln Asn Pro Asp Ser Ala
130 135

<210> 182
<211> 2155
<212> DNA
<213> *Bacillus licheniformis*

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<220>
<221> CDS
<222> (501)..(1655)
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[illegible]

10295.204.ST25.txt

ata ctc aat caa ttt cag cat aaa agg ttc tcc ttc gcc gag agc atc Ile Leu Asn Gln Phe Gln His Lys Arg Phe Ser Phe Ala Glu Ser Ile 125 130 135	917
att ccg acg gga aaa atc atg atg tac acg gtg att ccg ttt ttc ttt Ile Pro Thr Gly Lys Ile Met Met Tyr Thr Val Ile Pro Phe Phe 140 145 150 155	965
ata ttg gtt cag cca gat tta ggg tcc gca ttg gtg att tta tcg atc Ile Leu Val Gln Pro Asp Leu Gly Ser Ala Leu Val Ile Leu Ser Ile 160 165 170	1013
gca ttc acg ttg atg ctg gtc tcg ggg att tcg ggc agg atg atc gtg Ala Phe Thr Leu Met Leu Val Ser Gly Ile Ser Gly Arg Met Ile Val 175 180 185	1061
tcc ctg tca ctt gga ttc atg gca ttg gtt gcc ttt ttg acg tat ttg Ser Leu Ser Leu Gly Phe Met Ala Leu Val Ala Phe Leu Thr Tyr Leu 190 195 200	1109
cac aat cat tac ttt gag ata ttt tca aag att att aag cct cac cag His Asn His Tyr Phe Glu Ile Phe Ser Lys Ile Ile Lys Pro His Gln 205 210 215	1157
ctt gac cgg ata tat ggc tgg ctc agt cct cat gaa cat gcc tct aca Leu Asp Arg Ile Tyr Gly Trp Leu Ser Pro His Glu His Ala Ser Thr 220 225 230 235	1205
tat gga tac cag ctg acg cag gcg tta ttg ggg atc gga tca ggc cag Tyr Gly Tyr Gln Leu Thr Gln Ala Leu Leu Gly Ile Gly Ser Gly Gln 240 245 250	1253
ctg tca ggg agc ggc ttt act caa gga atc caa gtt cag gga ggg aaa Leu Ser Gly Ser Gly Phe Thr Gln Gly Ile Gln Val Gln Gly Gly Lys 255 260 265	1301
att ccg gag gct cat act gat ttt att ttc gcc gtg att ggt gag gaa Ile Pro Glu Ala His Thr Asp Phe Ile Phe Ala Val Ile Gly Glu Glu 270 275 280	1349
ttc ggt ttt ttg ggt gcc gta aca tta gtc tgt ctg tat ttt ctg atg Phe Gly Phe Leu Gly Ala Val Thr Leu Val Cys Leu Tyr Phe Leu Met 285 290 295	1397
atc tac aga atc atc agg att gcg ctt tcg tcc aac agt ctg ttc ggt Ile Tyr Arg Ile Ile Arg Ile Ala Leu Ser Ser Asn Ser Leu Phe Gly 300 305 310 315	1445
ctt tat ata tgt gcg ggg gtt gca ggg ttg att gta ttc caa gtg ttc Leu Tyr Ile Cys Ala Gly Val Ala Gly Leu Ile Val Phe Gln Val Phe 320 325 330	1493
caa aat atc ggg atg acg atc ggg tta atg ccg atc acg ggg ctc gct Gln Asn Ile Gly Met Thr Ile Gly Leu Met Pro Ile Thr Gly Leu Ala 335 340 345	1541
ctt ccg ttt atc agc tat ggc ggc agc gcg ctg ttg acc aac atg atc Leu Pro Phe Ile Ser Tyr Gly Gly Ser Ala Leu Leu Thr Asn Met Ile 350 355 360	1589
gct tta ggt ctc gtt ttc agt gtg aat atc aga tct aaa cat tac atg Ala Leu Gly Leu Val Phe Ser Val Asn Ile Arg Ser Lys His Tyr Met 365 370 375	1637
ttt ggg aat gat tgg gga tgaagttgct caaaatgatt ctttcccatc Phe Gly Asn Asp Trp Gly 380 385	1685

10295.204.ST25.txt

taaagaaact tgattatgta ttgattgccg cggttctgtt tttatctgcg tttggcttgc 1745
 tgatgggtata cagcgccggc taccctctcg gatatatgaa gtatcatgat ggcagctatt 1805
 tttttatgaa gcagctgcaa tggctgctca tcggtttggc ctttttttcg gctgccgcca 1865
 ttttcccata caaagcttac agcaaactca ttcggttttt ggtgaagctt tcttttttaa 1925
 tgctgattct cgttttgctg ccgggaatcg ggatggagaa aaacaattcc caaaggtgga 1985
 ttcaattcgg ttcgctcatg attcagccgt ctgaggctgt gaagcttgtg atgggtattt 2045
 atttcgccta tgtgtatgca aaaaagcaga aatacatcgc cgatttcgga aagggcgta 2105
 tgccgccgct gctgattttg gcggctgtgt ttttttgat tttaaaacag 2155

<210> 183
 <211> 385
 <212> PRT
 <213> Bacillus licheniformis

<400> 183

Met Lys Arg Lys His Ile Asn Ile Asp Ile Ser Leu Leu Leu Ile Leu
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Phe Cys Leu Phe Ile Ile Ser Leu Leu Ala Val Tyr Ser Gly Ser Gly
 20 25 30

Gln Tyr Glu Thr Gln Asp Pro Phe Tyr Phe Ala Lys Arg Gln Val Phe
 35 40 45

Trp Tyr Leu Val Gly Phe Gly Val Met Ala Gly Thr Ala Tyr Ile Asp
 50 55 60

Tyr Glu Leu Leu Glu Arg Leu Ala Leu Arg Leu Phe Val Gly Ala Val
 65 70 75 80

Phe Leu Leu Ile Leu Val His Phe Phe Gly Thr Tyr Lys Asn Gly Ser
 85 90 95

Gln Arg Trp Ile Ser Phe Gly Val Ile Glu Ile Gln Pro Ser Glu Phe
 100 105 110

Met Lys Ile Ile Leu Ile Leu Leu Leu Ala Ser Ile Leu Asn Gln Phe
 115 120 125

Gln His Lys Arg Phe Ser Phe Ala Glu Ser Ile Ile Pro Thr Gly Lys
 130 135 140

Ile Met Met Tyr Thr Val Ile Pro Phe Phe Phe Ile Leu Val Gln Pro
 145 150 155 160

Asp Leu Gly Ser Ala Leu Val Ile Leu Ser Ile Ala Phe Thr Leu Met
 165 170 175

10295.204.ST25.txt

Leu Val Ser Gly Ile Ser Gly Arg Met Ile Val Ser Leu Ser Leu Gly
 180 185 190
 Phe Met Ala Leu Val Ala Phe Leu Thr Tyr Leu His Asn His Tyr Phe
 195 200 205
 Glu Ile Phe Ser Lys Ile Ile Lys Pro His Gln Leu Asp Arg Ile Tyr
 210 215 220
 Gly Trp Leu Ser Pro His Glu His Ala Ser Thr Tyr Gly Tyr Gln Leu
 225 230 235 240
 Thr Gln Ala Leu Leu Gly Ile Gly Ser Gly Gln Leu Ser Gly Ser Gly
 245 250 255
 Phe Thr Gln Gly Ile Gln Val Gln Gly Gly Lys Ile Pro Glu Ala His
 260 265 270
 Thr Asp Phe Ile Phe Ala Val Ile Gly Glu Glu Phe Gly Phe Leu Gly
 275 280 285
 Ala Val Thr Leu Val Cys Leu Tyr Phe Leu Met Ile Tyr Arg Ile Ile
 290 295 300
 Arg Ile Ala Leu Ser Ser Asn Ser Leu Phe Gly Leu Tyr Ile Cys Ala
 305 310 315 320
 Gly Val Ala Gly Leu Ile Val Phe Gln Val Phe Gln Asn Ile Gly Met
 325 330 335
 Thr Ile Gly Leu Met Pro Ile Thr Gly Leu Ala Leu Pro Phe Ile Ser
 340 345 350
 Tyr Gly Gly Ser Ala Leu Leu Thr Asn Met Ile Ala Leu Gly Leu Val
 355 360 365
 Phe Ser Val Asn Ile Arg Ser Lys His Tyr Met Phe Gly Asn Asp Trp
 370 375 380

Gly
 385

<210> 184
 <211> 2113
 <212> DNA
 <213> Bacillus licheniformis

<220>
 <221> CDS
 <222> (501)..(1613)

<400> 184

10295.204.ST25.txt

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cgtcgcgacg atcaaaaaca gactgtttta caatgacagc aaagcgacaa acattcttgc	120
gacgaaaaaa gcgctgtccg cttttcaaaa gccggtcatt ttgctggcag gggggcttga	180
ccgcgggaaat gaatttgatg aactaaagcc gcatatgtct tttgtaaaag cggtgatcac	240
tttcggcgag accgcgccga agtttgagaa gctggccgaa gaaatgggaa tacaacaggt	300
taaacgtgtc gataatgttg aacaagcagc aactgcggcg ttcagcctgt cagacgaagg	360
agatgtcatt cttctgtccc cggcctgcgc aagctgggat cagtacaaaa catttgaaga	420
acgtggtgac atgtttgtaa acgccgtgca tatgcttaaa taagggcttg tctcgtaaag	480
atagccctaa gaattagagc ttg ggg tgt tgc gct ttg caa aca aaa aaa acg	533
Leu Gly Cys Ser Ala Leu Gln Thr Lys Lys Thr	
1 5 10	
tca ccg gat ttt ttg ctg gtt atc att acg cta ttg ctt tta aca atc	581
Ser Pro Asp Phe Leu Leu Val Ile Ile Thr Leu Leu Leu Leu Thr Ile	
15 20 25	
gga ctg att atg gta tac agc gcc agt gca gta tgg gcg act tac aaa	629
Gly Leu Ile Met Val Tyr Ser Ala Ser Ala Val Trp Ala Thr Tyr Lys	
30 35 40	
tac gac gac tcc ttt ttc ttt gcg aaa cgg cag ctt ttg ttt gcc ggc	677
Tyr Asp Asp Ser Phe Phe Phe Ala Lys Arg Gln Leu Leu Phe Ala Gly	
45 50 55	
atc ggg gtc atc gcc atg ttt ttc atc atg aac gtc gac tac tgg acg	725
Ile Gly Val Ile Ala Met Phe Phe Ile Met Asn Val Asp Tyr Trp Thr	
60 65 70 75	
tgg agg act tat gcg aaa ata ctg atc att gta tgt ttc ttt ctg ctc	773
Trp Arg Thr Tyr Ala Lys Ile Leu Ile Ile Val Cys Phe Phe Leu Leu	
80 85 90	
atc atc gtc ctg gtt ccc ggg atc ggc atg gaa cgg aac ggg tgc agg	821
Ile Ile Val Leu Val Pro Gly Ile Gly Met Glu Arg Asn Gly Ser Arg	
95 100 105	
agc tgg atc gga gtc ggc gct ttc agc att cag ccg tcc gag ttt atg	869
Ser Trp Ile Gly Val Gly Ala Phe Ser Ile Gln Pro Ser Glu Phe Met	
110 115 120	
aaa ctc gcg atg atc gca ttt ttg gcc aag ttt tta tct gaa aag caa	917
Lys Leu Ala Met Ile Ala Phe Leu Ala Lys Phe Leu Ser Glu Lys Gln	
125 130 135	
aag aat att acg tgc ttt aga aaa ggc ttt gtg ccg gcg ctg ggc att	965
Lys Asn Ile Thr Ser Phe Arg Lys Gly Phe Val Pro Ala Leu Gly Ile	
140 145 150 155	
gtc ttt tca gct ttt ctg atc atc atg atg cag cct gac ctc gga aca	1013
Val Phe Ser Ala Phe Leu Ile Ile Met Met Gln Pro Asp Leu Gly Thr	
160 165 170	
gga acc gtg atg gtc ggc aca tgc atc att atg atc ttt gtc gcg ggg	1061
Gly Thr Val Met Val Gly Thr Cys Ile Ile Met Ile Phe Val Ala Gly	
175 180 185	
gcg aga att tgc cac ttc gtt ttt ctc ggc ctg atc gga ctg agc ggt	1109
Ala Arg Ile Ser His Phe Val Phe Leu Gly Leu Ile Gly Leu Ser Gly	
190 195 200	

10295.204.ST25.txt

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ttt gtc ggc ctt gtg ctg tcg gcg ccg tac cgg atc aaa agg atc act 1157
Phe Val Gly Leu Val Leu Ser Ala Pro Tyr Arg Ile Lys Arg Ile Thr
205 210 215

tca tac ttg aac cct tgg gag gac cct tta gga agc ggc ttt caa atc 1205
Ser Tyr Leu Asn Pro Trp Glu Asp Pro Leu Gly Ser Gly Phe Gln Ile
220 225 230 235

att cag tct ctt tat gcg gtg ggg ccc ggc ggg ctg ttc ggc ctc ggc 1253
Ile Gln Ser Leu Tyr Ala Val Gly Pro Gly Gly Leu Phe Gly Leu Gly
240 245 250

ctc ggc cag agc agg caa aag ttt ttc tat ctg cct gag ccg cag aca 1301
Leu Gly Gln Ser Arg Gln Lys Phe Phe Tyr Leu Pro Glu Pro Gln Thr
255 260 265

gat ttt att ttt gcg att tta tca gag gag ctc ggc ttt atc ggc gga 1349
Asp Phe Ile Phe Ala Ile Leu Ser Glu Glu Leu Gly Phe Ile Gly Gly
270 275 280

tcg ctg att ctt ttg ctc ttc agc gtt cta tta tgg aga ggc atc aga 1397
Ser Leu Ile Leu Leu Leu Phe Ser Val Leu Leu Trp Arg Gly Ile Arg
285 290 295

atc gcg ctc ggt gcg ccc gat tta tac ggc agt ttt gtc gcc gtc ggc 1445
Ile Ala Leu Gly Ala Pro Asp Leu Tyr Gly Ser Phe Val Ala Val Gly
300 305 310 315

gtc att tcg atg ata gcg att cag gtt atg atc aat atc gga gtc gtg 1493
Val Ile Ser Met Ile Ala Ile Gln Val Met Ile Asn Ile Gly Val Val
320 325 330

act ggt ttg att cct gtt aca ggc att acg ctt ccg ttt tta agc tat 1541
Thr Gly Leu Ile Pro Val Thr Gly Ile Thr Leu Pro Phe Leu Ser Tyr
335 340 345

ggc ggt tca tca ctg acc ttg atg ctc atg gcg gtc ggc gtg ctg ctg 1589
Gly Gly Ser Ser Leu Thr Leu Met Leu Met Ala Val Gly Val Leu Leu
350 355 360

aat gtc agc agg tat tct aga tac tagatTTTtgg cgataaccct gttgCGagat 1643
Asn Val Ser Arg Tyr Ser Arg Tyr
365 370

agcaggggtta tcggcgtgta cataaggatt aaggggggaga acagatgcgg attgttgTTa 1703

gcggaggcgcg aacggggcggc catattttacc ccgcccttgc gtttattaaa gaagtgaAAC 1763

ggcatcacga agatgttgag tttttatata tcggaaccga aaaaggcctg gagaaaaata 1823

tcgtcgagcg ggaagggatc cttttcaaag cgattgaaat tacgggtttt aaaagaaaac 1883

tttcatttga aaacgtcaaa accgtcatgc gctttttaaa ggggtgtaaaa gaatgcaaag 1943

aagaattaaa acggttcaag ccggatgccg tgatcggcac gggcggctac gtgtgcggcc 2003

ccgtcgtata cgccgcttca aaactgggga ttccgacgat tatccacgaa caaaacagcc 2063

ttcccggact caccaataag tttttatcca aatatgttga taaggtagcg 2113

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<210> 185

<211> 371

<212> PRT

<213> Bacillus licheniformis

<400> 185

10295.204.ST25.txt

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 Leu Val Ile Ile Thr Leu Leu Leu Leu Thr Ile Gly Leu Ile Met Val
 20 25 30
 Tyr Ser Ala Ser Ala Val Trp Ala Thr Tyr Lys Tyr Asp Asp Ser Phe
 35 40 45
 Phe Phe Ala Lys Arg Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala
 50 55 60
 Met Phe Phe Ile Met Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala
 65 70 75 80
 Lys Ile Leu Ile Ile Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val
 85 90 95
 Pro Gly Ile Gly Met Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val
 100 105 110
 Gly Ala Phe Ser Ile Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile
 115 120 125
 Ala Phe Leu Ala Lys Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser
 130 135 140
 Phe Arg Lys Gly Phe Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe
 145 150 155 160
 Leu Ile Ile Met Met Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val
 165 170 175
 Gly Thr Cys Ile Ile Met Ile Phe Val Ala Gly Ala Arg Ile Ser His
 180 185 190
 Phe Val Phe Leu Gly Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val
 195 200 205
 Leu Ser Ala Pro Tyr Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro
 210 215 220
 Trp Glu Asp Pro Leu Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr
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 Ala Val Gly Pro Gly Gly Leu Phe Gly Leu Gly Leu Gly Gln Ser Arg
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 Gln Lys Phe Phe Tyr Leu Pro Glu Pro Gln Thr Asp Phe Ile Phe Ala
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10295.204.ST25.txt

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Pro Asp Leu Tyr Gly Ser Phe Val Ala Val Gly Val Ile Ser Met Ile
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Ala Ile Gln Val Met Ile Asn Ile Gly Val Val Thr Gly Leu Ile Pro
 325 330 335

Val Thr Gly Ile Thr Leu Pro Phe Leu Ser Tyr Gly Gly Ser Ser Leu
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 Glu Arg Thr Gly Gly Asp Ile Tyr Leu Gly Val Val Gly Ala Val Arg
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 Thr Gly Lys Ser Thr Phe Ile Lys Lys Phe Met Glu Leu Val Val Leu
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 Page 279

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 Pro Glu Ile Ile Arg Gln Gly Ser Arg Phe Gly Val Arg Leu Lys Ala
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 Ala Pro Ile Ile Gly Thr Glu Lys Gln Ser Glu Glu Leu Val Arg Tyr
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10295.204.ST25.txt

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355 360 365

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370 375 380

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385 390 395 400

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Leu Ser Ser Ile Val Arg Glu Gly Ile Gln Ala Lys Leu Ser Leu Met
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Lys Gly Pro Val Thr Leu Glu Lys Gln Lys Asp Ser Asp Ala Leu Asn	
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10295.204.ST25.txt

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gcc Ala 655	gtg Val 655	ccg Pro 655	atc Ile 655	ggc Gly 655	tat Tyr 655	aaa Lys 655	gga Gly 660	aaa Lys 660	gac Asp 660	gac Asp 660	att Ile 660	gtt Val 665	tat Tyr 665	tta Leu 665	aac Asn 665	2501
ctt Leu 670	cac His 670	gaa Glu 670	aag Lys 670	gcg Ala 670	cac His 670	ggc Gly 675	ccc Pro 675	cac His 675	ggg Gly 675	ctg Leu 675	ctt Leu 675	gcc Ala 680	gga Gly 680	acg Thr 680	acc Thr 680	2549
ggc Gly 685	tcg Ser 685	ggc Gly 685	aaa Lys 685	agt Ser 685	gaa Glu 685	ttt Phe 690	ttg Leu 690	cag Gln 690	act Thr 690	tat Tyr 690	att Ile 695	ttg Leu 695	tct Ser 695	ttg Leu 695	gca Ala 695	2597
gtt Val 700	cac His 700	ttt Phe 700	cac His 700	ccg Pro 700	cat His 705	gaa Glu 705	gtc Val 705	gca Ala 705	ttt Phe 710	ttg Leu 710	cta Leu 710	atc Ile 710	gac Asp 710	tac Tyr 715	aaa Lys 715	2645
ggg Gly 720	ggc Gly 720	gga Gly 720	atg Met 720	gcg Ala 720	cag Gln 720	ccg Pro 720	ttc Phe 720	cgg Arg 725	aac Asn 725	att Ile 725	ccg Pro 725	cat His 725	ttg Leu 730	ctc Leu 730	gga Gly 730	2693
acg Thr 735	att Ile 735	act Thr 735	aac Asn 735	att Ile 735	gaa Glu 735	ggc Gly 735	agc Ser 740	aag Lys 740	aac Asn 740	ttc Phe 740	agc Ser 745	aac Asn 745	cgg Arg 745	gcg Ala 745	ctt Leu 745	2741
gcg Ala 750	tcc Ser 750	att Ile 750	aag Lys 750	agc Ser 750	gag Glu 750	ctg Leu 755	aag Lys 755	aaa Lys 755	agg Arg 755	cag Gln 755	cgg Arg 760	ctc Leu 760	ttt Phe 760	gat Asp 760	cag Gln 760	2789
tac Tyr 765	aaa Lys 765	gtg Val 765	aac Asn 765	cat His 765	atc Ile 765	aac Asn 770	gac Asp 770	tat Tyr 770	aca Thr 770	aag Lys 775	ctt Leu 775	tac Tyr 775	aaa Lys 775	cag Gln 775	aaa Lys 775	2837
aaa Lys 780	gcg Ala 780	aaa Lys 780	acg Thr 780	gcg Ala 780	atg Met 785	ccg Pro 785	cac His 785	ctt Leu 785	ttc Phe 785	tta Leu 790	att Ile 790	tca Ser 790	gac Asp 790	gaa Glu 790	ttt Phe 795	2885

10295.204.ST25.txt

gcc	gag	ctg	aaa	agc	gaa	gaa	ccg	gaa	ttt	atc	cgc	gag	ctt	gtc	agt	2933
Ala	Glu	Leu	Lys	Ser	Glu	Glu	Pro	Glu	Phe	Ile	Arg	Glu	Leu	Val	Ser	
				800					805					810		
gcg	gca	agg	atc	ggg	cga	agc	ctc	ggg	gtg	cac	tta	atc	ttg	gcg	acg	2981
Ala	Ala	Arg	Ile	Gly	Arg	Ser	Leu	Gly	Val	His	Leu	Ile	Leu	Ala	Thr	
			815					820					825			
caa	aaa	ccg	ggc	ggc	atc	atc	gat	gac	cag	att	tgg	agc	aac	tcc	aga	3029
Gln	Lys	Pro	Gly	Gly	Ile	Ile	Asp	Asp	Gln	Ile	Trp	Ser	Asn	Ser	Arg	
		830					835					840				
ttc	aag	gtc	gcc	ttg	aag	gtg	cag	gat	gcg	aat	gac	agt	aaa	gag	atc	3077
Phe	Lys	Val	Ala	Leu	Lys	Val	Gln	Asp	Ala	Asn	Asp	Ser	Lys	Glu	Ile	
	845					850					855					
ctc	aaa	aac	ggg	gat	gcg	gct	acc	atc	acg	gta	acg	ggc	cgc	ggc	tat	3125
Leu	Lys	Asn	Gly	Asp	Ala	Ala	Thr	Ile	Thr	Val	Thr	Gly	Arg	Gly	Tyr	
	860				865					870					875	
ttg	caa	gtc	ggc	aac	aac	gag	gtg	tat	gaa	ctg	ttc	cag	tct	gca	tgg	3173
Leu	Gln	Val	Gly	Asn	Asn	Glu	Val	Tyr	Glu	Leu	Phe	Gln	Ser	Ala	Trp	
				880					885					890		
agc	gga	gcc	cct	tac	atg	gag	gac	ggc	tac	ggc	aca	gag	gat	gaa	gtg	3221
Ser	Gly	Ala	Pro	Tyr	Met	Glu	Asp	Gly	Tyr	Gly	Thr	Glu	Asp	Glu	Val	
			895					900					905			
gcg	atc	gtc	aca	gat	acc	gga	tta	att	cct	tta	tca	gat	gtt	gat	gct	3269
Ala	Ile	Val	Thr	Asp	Thr	Gly	Leu	Ile	Pro	Leu	Ser	Asp	Val	Asp	Ala	
		910					915					920				
gat	cgc	gct	gcg	aaa	aaa	gag	gct	gtg	acg	gaa	att	tcg	gca	gtc	gtc	3317
Asp	Arg	Ala	Ala	Lys	Lys	Glu	Ala	Val	Thr	Glu	Ile	Ser	Ala	Val	Val	
	925					930					935					
gaa	caa	att	gaa	cgg	att	caa	gcg	gag	atg	gga	atc	gag	aag	ctc	ccg	3365
Glu	Gln	Ile	Glu	Arg	Ile	Gln	Ala	Glu	Met	Gly	Ile	Glu	Lys	Leu	Pro	
	940				945					950					955	
agc	cct	tgg	ctg	ccg	ccg	ctt	gaa	gaa	cgc	ata	ccg	aaa	acg	cgc	tat	3413
Ser	Pro	Trp	Leu	Pro	Pro	Leu	Glu	Glu	Arg	Ile	Pro	Lys	Thr	Arg	Tyr	
				960					965					970		
ccg	tcg	gag	gaa	gcc	gat	gcc	ttt	aac	ttt	gcc	tat	atc	gat	gaa	cct	3461
Pro	Ser	Glu	Glu	Ala	Asp	Ala	Phe	Asn	Phe	Ala	Tyr	Ile	Asp	Glu	Pro	
			975					980					985			
gaa	aag	caa	agc	cag	gag	ccg	atc	agc	tac	cgc	atg	atg	gaa	gac	ggc	3509
Glu	Lys	Gln	Ser	Gln	Glu	Pro	Ile	Ser	Tyr	Arg	Met	Met	Glu	Asp	Gly	
		990					995					1000				
aat	atc	ggc	atc	gtc	ggc	tcg	tca	ggc	tac	gga	aaa	tcc	ctg	aca		3554
Asn	Ile	Gly	Ile	Val	Gly	Ser	Ser	Gly	Tyr	Gly	Lys	Ser	Leu	Thr		
	1005					1010					1015					
gcc	acg	acg	ttc	atg	atg	agc	ttt	gcc	gaa	cag	tat	acg	ccg	gaa		3599
Ala	Thr	Thr	Phe	Met	Met	Ser	Phe	Ala	Glu	Gln	Tyr	Thr	Pro	Glu		
	1020					1025					1030					
gaa	ttg	cat	tac	tac	att	ttc	gac	ttt	ggc	aac	gga	acg	ctg	ctt		3644
Glu	Leu	His	Tyr	Tyr	Ile	Phe	Asp	Phe	Gly	Asn	Gly	Thr	Leu	Leu		
	1035					1040					1045					
ccg	ctt	gca	agg	ctt	ccg	cac	acc	gcg	gat	tat	ttc	ctg	atg	gac		3689
Pro	Leu	Ala	Arg	Leu	Pro	His	Thr	Ala	Asp	Tyr	Phe	Leu	Met	Asp		
	1050					1055					1060					

10295.204.ST25.txt

caa Gln	acg Thr	aga Arg	aaa Lys	atc Ile	gag Glu	aaa Lys	ttt Phe	atg Met	gtc Val	cgg Arg	atc Ile	aag Lys	gcg Ala	gaa Glu	3734
1065						1070					1075				
atc Ile	gag Glu	cac His	agg Arg	aaa Lys	aat Asn	ctc Leu	ttc Phe	cgt Arg	gca Ala	aaa Lys	gaa Glu	atc Ile	agc Ser	cat His	3779
1080						1085					1090				
atc Ile	aag Lys	atg Met	tac Tyr	aat Asn	gcg Ala	ctg Leu	aat Asn	gag Glu	gaa Glu	aag Lys	ctg Leu	ccg Pro	ttt Phe	att Ile	3824
1095						1100					1105				
ttc Phe	ata Ile	acg Thr	gtc Val	gac Asp	aac Asn	ttt Phe	gac Asp	atc Ile	att Ile	aaa Lys	gac Asp	gaa Glu	atg Met	cat His	3869
1110						1115					1120				
gaa Glu	ctc Leu	gaa Glu	agc Ser	gaa Glu	ttt Phe	atc Ile	cag Gln	ttt Phe	tca Ser	cga Arg	gac Asp	ggc Gly	cag Gln	tcg Ser	3914
1125						1130					1135				
ctt Leu	gga Gly	att Ile	tat Tyr	tta Leu	atc Ile	ctg Leu	acc Thr	gcg Ala	aca Thr	agg Arg	gtc Val	aat Asn	gca Ala	atc Ile	3959
1140						1145					1150				
aga Arg	cag Gln	tcg Ser	ctc Leu	ttg Leu	aac Asn	aac Asn	ctg Leu	aaa Lys	acg Thr	agg Arg	gtt Val	gtc Val	cac His	tat Tyr	4004
1155						1160					1165				
ctg Leu	atg Met	gat Asp	cag Gln	tct Ser	gaa Glu	gca Ala	tat Tyr	tcg Ser	att Ile	atc Ile	gga Gly	agg Arg	ccg Pro	gaa Glu	4049
1170						1175					1180				
ttc Phe	agc Ser	ctt Leu	gaa Glu	ccg Pro	atc Ile	cct Pro	gga Gly	cgc Arg	gtt Val	att Ile	atc Ile	aat Asn	aaa Lys	gaa Glu	4094
1185						1190					1195				
aac Asn	caa Gln	tac Tyr	ttc Phe	gca Ala	caa Gln	atg Met	ttt Phe	atg Met	cct Pro	gtg Val	gaa Glu	gcg Ala	gac Asp	aac Asn	4139
1200						1205					1210				
gat Asp	atc Ile	gag Glu	ctg Leu	ttt Phe	gaa Glu	ggg Gly	atc Ile	aaa Lys	gcc Ala	gac Asp	att Ile	cag Gln	gcg Ala	atc Ile	4184
1215						1220					1225				
gca Ala	gaa Glu	cgc Arg	tcg Ser	gaa Glu	ggc Gly	atg Met	aga Arg	aag Lys	ccg Pro	gcg Ala	cct Pro	gtg Val	ccg Pro	atg Met	4229
1230						1235					1240				
ctg Leu	ccg Pro	ctc Leu	gag Glu	ctt Leu	tcc Ser	gtc Val	aca Thr	cag Gln	ttt Phe	gtg Val	aga Arg	gat Asp	tat Tyr	ccg Pro	4274
1245						1250					1255				
ctt Leu	cag Gln	cct Pro	gaa Glu	aga Arg	ggc Gly	ctt Leu	att Ile	cca Pro	atg Met	gga Gly	ctc Leu	gat Asp	gaa Glu	gaa Glu	4319
1260						1265					1270				
act Thr	gtc Val	gaa Glu	ccc Pro	gta Val	tac Tyr	ttt Phe	aat Asn	ctt Leu	gag Glu	aaa Lys	aat Asn	aag Lys	cac His	tgc Cys	4364
1275						1280					1285				
ctc Leu	att Ile	atg Met	ggt Gly	cag Gln	acg Thr	cag Gln	cgc Arg	gga Gly	aaa Lys	aca Thr	aac Asn	gtc Val	atc Ile	aag Lys	4409
1290						1295					1300				
atc Ile	atg Met	ctc Leu	gag Glu	cac His	ctg Leu	ctt Leu	gac Asp	cat His	gac Asp	acg Thr	aaa Lys	aaa Lys	atc Ile	gcc Ala	4454
1305						1310					1315				

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gtg ttt gat tcg ata gac aga	ggg ctt tct caa tat	gcg aca gag	4499
Val Phe Asp Ser Ile Asp Arg	Gly Leu Ser Gln Tyr	Ala Thr Glu	
1320	1325	1330	
gat caa atc agc tat cta gaa	aca aaa gac gac att	ctg ctc tgg	4544
Asp Gln Ile Ser Tyr Leu Glu	Thr Lys Asp Asp Ile	Leu Leu Trp	
1335	1340	1345	
ctc gct gag acg gaa gaa att	tgc cgg aca agg gaa	gcg atg tat	4589
Leu Ala Glu Thr Glu Glu Ile	Cys Arg Thr Arg Glu	Ala Met Tyr	
1350	1355	1360	
ttg gaa gcc gtt aaa caa gga	gaa atc gcc aac ctt	gat ttc tca	4634
Leu Glu Ala Val Lys Gln Gly	Glu Ile Ala Asn Leu	Asp Phe Ser	
1365	1370	1375	
ccg atg gtc ttt att gtc gac	gga att tca cgg ttc	cag cag acg	4679
Pro Met Val Phe Ile Val Asp	Gly Ile Ser Arg Phe	Gln Gln Thr	
1380	1385	1390	
atc gac gca tcg att cag gac	aaa atg gcg atg ttc	atg aaa tct	4724
Ile Asp Ala Ser Ile Gln Asp	Lys Met Ala Met Phe	Met Lys Ser	
1395	1400	1405	
tac gcc cat tta ggt ttc cac	ttt ata cct gcc gga	aat cac agc	4769
Tyr Ala His Leu Gly Phe His	Phe Ile Pro Ala Gly	Asn His Ser	
1410	1415	1420	
gag ttc aca aaa ggc tat gat	tcg ctg aca agc gaa	gtc aag cag	4814
Glu Phe Thr Lys Gly Tyr Asp	Ser Leu Thr Ser Glu	Val Lys Gln	
1425	1430	1435	
gtc aga cac gcg atg cta ttg	atg aaa aaa tcc gag	cag aac ttg	4859
Val Arg His Ala Met Leu Leu	Met Lys Lys Ser Glu	Gln Asn Leu	
1440	1445	1450	
att cag ctc cca tat gaa cgc	cag gag ccg gaa att	ctg ccg ggc	4904
Ile Gln Leu Pro Tyr Glu Arg	Gln Glu Pro Glu Ile	Leu Pro Gly	
1455	1460	1465	
ttt ggc tat atc gtt gaa aac	ggc aaa gag agg aaa	att caa att	4949
Phe Gly Tyr Ile Val Glu Asn	Gly Lys Glu Arg Lys	Ile Gln Ile	
1470	1475	1480	
cct tta tgt gct gta gaa agg	aag aaa gcg aaa tgacggaaca		4992
Pro Leu Cys Ala Val Glu Arg	Lys Lys Ala Lys		
1485	1490		
acaaaaaagc acgctgaaaa ttatcagcgc catcgtcacg atcatcttg	tgcccgtcct		5052
gttttttcat ttcacggtg agaaccgcgac gaaaaaggta tcgaacgcga	caagggaaat		5112
cgccgttggtc aatgaggata ccggcgtttt gaaagatgac ggaaccgttg	atcaagatgc		5172
gctgctggga aacgaaatct cggcttcctt ggttgaccgt ccggattata	aatggacggt		5232
cgtcaaccgg agcgcagcag aaagcggact tgcggagaag caatacgatg	cgattgtcta		5292
cattccgtcg gacttttcgc aaaacatttt aagctacaac catgagcgtc	cgcaaaaagc		5352
ggagctggaa ttcaaaaattc aggaccagct cgacgccgtc aacaaggaaa	aagtccagcg		5412
cgagcttcag gacgcgcaaa aaacggtgag caagaaaatg tcttccctgt	actggcgctt		5472
tgtcaaacag			5482

10295.204.ST25.txt

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<400> 189

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Leu Asp Asp Gln Asn Ser Arg Thr Leu Thr Ile Gly Pro Asp Leu Lys
 20 25 30

His Ser Val Thr Ile Lys His Phe Ser Phe Glu Lys Gly Pro Val Thr
 35 40 45

Leu Glu Lys Gln Lys Asp Ser Asp Ala Leu Asn Val Gln Leu Gly Gly
 50 55 60

Glu Thr Val Ser Ser Leu Lys Leu Gly Gly Lys Ala Ser Val Gln Ser
 65 70 75 80

Gly Ala Glu Gln Leu Thr Leu Phe Leu Ala Glu Glu Ala Asp Ser Val
 85 90 95

Pro Ala Tyr Tyr Leu Gly Glu Arg Gln Glu Ile Val Ile Ser Ser Leu
 100 105 110

Asp Gln Glu Ala Asp Val Tyr Phe Asn Glu Thr Asp Ser Phe Phe Gly
 115 120 125

Glu Lys Gly Thr Phe Ser Phe Ile Arg Leu Asp Gly Gln Trp Asn Val
 130 135 140

Leu Pro Asn Asp Ala Lys Ile Tyr Leu Asn Gly Glu Glu Val Ser Ala
 145 150 155 160

Pro Val Ser Val Gln Asn Gly Asp Glu Ile Ala Phe Gly Leu Asn Ile
 165 170 175

Leu Arg Ile Val Glu Asp Asp Leu Leu Glu Ile Glu Gly Phe Gly Lys
 180 185 190

Phe Asp Thr Ser Leu Glu Asn Ile Leu Lys Pro Ser Ser Glu Thr Lys
 195 200 205

Asn Lys Tyr Pro Gln Tyr Arg Arg Pro Pro Arg Met Ile Tyr Asp Leu
 210 215 220

Pro Asp Glu Lys Val Ser Phe Ser Phe Pro Ala Gln Glu Ser Asp Gly
 225 230 235 240

Asp Asn Arg Gly Leu Trp Leu Met Ile Leu Pro Pro Leu Val Met Leu
 245 250 255

10295.204.ST25.txt

Ile Val Met Gly Ile Val Ala Leu Ile Gln Pro Arg Gly Ile Phe Ile
 260 265 270

Ile Val Ser Leu Ala Met Phe Met Met Thr Leu Ile Thr Ser Thr Val
 275 280 285

Gln Tyr Phe Arg Asp Lys Asn Gln Arg Lys Lys Arg Glu Glu Lys Arg
 290 300

Glu Arg Val Tyr Thr Leu Tyr Leu Glu Asn Lys Lys Lys Glu Leu His
 305 310 315 320

Glu Leu Ala Glu Arg Gln Lys Phe Val Leu Asp Phe His Phe Pro Thr
 325 330 335

Phe Glu Arg Met Lys Tyr Leu Thr Lys Glu Ile Ser Gly Arg Ile Trp
 340 345 350

Glu Lys Ser Ile Glu Ser Ala Asp Phe Leu Gln Ile Arg Leu Gly Thr
 355 360 365

Gly Asn Val Ala Ser Ser Tyr Gln Ile Asn Leu Asn Gly Gly Asp Leu
 370 375 380

Ala Asn Arg Asp Thr Asp His Leu Leu Glu Gln Thr Gln Lys Met Glu
 385 390 400

Glu Val Tyr Arg Glu Leu Lys Asn Ala Pro Ile Thr Val Asn Leu Ala
 405 410 415

Glu Gly Pro Met Gly Val Val Gly Lys Leu Ser Val Val Lys Asn Glu
 420 425 430

Ile His Gln Leu Val Gly Gln Leu Ala Phe Phe His Ser Tyr His Asp
 435 440 445

Leu Arg Phe Val Phe Ile Phe Asp Glu Ala Glu Tyr Gln Glu Trp Glu
 450 455 460

Trp Met Lys Trp Leu Pro His Phe Gln Met Pro His Ile Tyr Ala Lys
 465 470 475 480

Gly Phe Ile Tyr Asn Glu Gln Thr Arg Asp Gln Leu Leu Ser Ser Ile
 485 490 495

Tyr Glu Ile Leu Arg Glu Arg Asp Leu Asp Glu Asn Lys Lys Lys Thr
 500 505 510

Leu Phe Lys Pro His Phe Val Phe Ile Ile Thr Asn Gln Gln Leu Ile
 515 520 525

10295.204.ST25.txt

Ala Glu His Val Ile Leu Glu Tyr Leu Glu Gly Lys Gln Lys His Leu
 530 535 540

Gly Val Ser Thr Ile Val Ala Ala Glu Thr Lys Glu Ser Leu Ser Glu
 545 550 555 560

Asn Ile His Thr Leu Val Arg Tyr Ile Thr Glu Gln Glu Gly Asp Ile
 565 570 575

Leu Ile Lys Gln Lys Lys Ala Val Gln Ile Pro Phe Gln Leu Asp His
 580 585 590

His Asn Arg Glu Asp Asn Glu Gln Phe Ser Arg Thr Leu Arg Thr Leu
 595 600 605

Asp His Gln Thr Gly Met Thr Asn Ser Ile Pro Asp Thr Val Ser Phe
 610 615 620

Leu Glu Leu Phe Gln Val Lys Glu Val Asp Asp Ile Gly Ile Glu Gln
 625 630 635 640

Lys Trp Met Thr Ser Glu Ser Ala Lys Ser Leu Ala Val Pro Ile Gly
 645 650 655

Tyr Lys Gly Lys Asp Asp Ile Val Tyr Leu Asn Leu His Glu Lys Ala
 660 665 670

His Gly Pro His Gly Leu Leu Ala Gly Thr Thr Gly Ser Gly Lys Ser
 675 680 685

Glu Phe Leu Gln Thr Tyr Ile Leu Ser Leu Ala Val His Phe His Pro
 690 695 700

His Glu Val Ala Phe Leu Leu Ile Asp Tyr Lys Gly Gly Gly Met Ala
 705 710 715 720

Gln Pro Phe Arg Asn Ile Pro His Leu Leu Gly Thr Ile Thr Asn Ile
 725 730 735

Glu Gly Ser Lys Asn Phe Ser Asn Arg Ala Leu Ala Ser Ile Lys Ser
 740 745 750

Glu Leu Lys Lys Arg Gln Arg Leu Phe Asp Gln Tyr Lys Val Asn His
 755 760 765

Ile Asn Asp Tyr Thr Lys Leu Tyr Lys Gln Lys Lys Ala Lys Thr Ala
 770 775 780

Met Pro His Leu Phe Leu Ile Ser Asp Glu Phe Ala Glu Leu Lys Ser
 785 790 795 800

10295.204.ST25.txt

Glu Glu Pro Glu Phe Ile Arg Glu Leu Val Ser Ala Ala Arg Ile Gly
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 Arg Ser Leu Gly Val His Leu Ile Leu Ala Thr Gln Lys Pro Gly Gly
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 Ile Ile Asp Asp Gln Ile Trp Ser Asn Ser Arg Phe Lys Val Ala Leu
 835 840 845
 Lys Val Gln Asp Ala Asn Asp Ser Lys Glu Ile Leu Lys Asn Gly Asp
 850 855 860
 Ala Ala Thr Ile Thr Val Thr Gly Arg Gly Tyr Leu Gln Val Gly Asn
 865 870 875 880
 Asn Glu Val Tyr Glu Leu Phe Gln Ser Ala Trp Ser Gly Ala Pro Tyr
 885 890 895
 Met Glu Asp Gly Tyr Gly Thr Glu Asp Glu Val Ala Ile Val Thr Asp
 900 905 910
 Thr Gly Leu Ile Pro Leu Ser Asp Val Asp Ala Asp Arg Ala Ala Lys
 915 920 925
 Lys Glu Ala Val Thr Glu Ile Ser Ala Val Val Glu Gln Ile Glu Arg
 930 935 940
 Ile Gln Ala Glu Met Gly Ile Glu Lys Leu Pro Ser Pro Trp Leu Pro
 945 950 955 960
 Pro Leu Glu Glu Arg Ile Pro Lys Thr Arg Tyr Pro Ser Glu Glu Ala
 965 970 975
 Asp Ala Phe Asn Phe Ala Tyr Ile Asp Glu Pro Glu Lys Gln Ser Gln
 980 985 990
 Glu Pro Ile Ser Tyr Arg Met Met Glu Asp Gly Asn Ile Gly Ile Val
 995 1000 1005
 Gly Ser Ser Gly Tyr Gly Lys Ser Leu Thr Ala Thr Thr Phe Met
 1010 1015 1020
 Met Ser Phe Ala Glu Gln Tyr Thr Pro Glu Glu Leu His Tyr Tyr
 1025 1030 1035
 Ile Phe Asp Phe Gly Asn Gly Thr Leu Leu Pro Leu Ala Arg Leu
 1040 1045 1050
 Pro His Thr Ala Asp Tyr Phe Leu Met Asp Gln Thr Arg Lys Ile
 1055 1060 1065

10295.204.ST25.txt

Glu Lys Phe Met Val Arg Ile Lys Ala Glu Ile Glu His Arg Lys
 1070 1075 1080
 Asn Leu Phe Arg Ala Lys Glu Ile Ser His Ile Lys Met Tyr Asn
 1085 1090 1095
 Ala Leu Asn Glu Glu Lys Leu Pro Phe Ile Phe Ile Thr Val Asp
 1100 1105 1110
 Asn Phe Asp Ile Ile Lys Asp Glu Met His Glu Leu Glu Ser Glu
 1115 1120 1125
 Phe Ile Gln Phe Ser Arg Asp Gly Gln Ser Leu Gly Ile Tyr Leu
 1130 1135 1140
 Ile Leu Thr Ala Thr Arg Val Asn Ala Ile Arg Gln Ser Leu Leu
 1145 1150 1155
 Asn Asn Leu Lys Thr Arg Val Val His Tyr Leu Met Asp Gln Ser
 1160 1165 1170
 Glu Ala Tyr Ser Ile Ile Gly Arg Pro Glu Phe Ser Leu Glu Pro
 1175 1180 1185
 Ile Pro Gly Arg Val Ile Ile Asn Lys Glu Asn Gln Tyr Phe Ala
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 Gln Met Phe Met Pro Val Glu Ala Asp Asn Asp Ile Glu Leu Phe
 1205 1210 1215
 Glu Gly Ile Lys Ala Asp Ile Gln Ala Ile Ala Glu Arg Ser Glu
 1220 1225 1230
 Gly Met Arg Lys Pro Ala Pro Val Pro Met Leu Pro Leu Glu Leu
 1235 1240 1245
 Ser Val Thr Gln Phe Val Arg Asp Tyr Pro Leu Gln Pro Glu Arg
 1250 1255 1260
 Gly Leu Ile Pro Met Gly Leu Asp Glu Glu Thr Val Glu Pro Val
 1265 1270 1275
 Tyr Phe Asn Leu Glu Lys Asn Lys His Cys Leu Ile Met Gly Gln
 1280 1285 1290
 Thr Gln Arg Gly Lys Thr Asn Val Ile Lys Ile Met Leu Glu His
 1295 1300 1305
 Leu Leu Asp His Asp Thr Lys Lys Ile Ala Val Phe Asp Ser Ile
 1310 1315 1320

10295.204.ST25.txt

Asp Arg Gly Leu Ser Gln Tyr Ala Thr Glu Asp Gln Ile Ser Tyr
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 Leu Glu Thr Lys Asp Asp Ile Leu Leu Trp Leu Ala Glu Thr Glu
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 Glu Ile Cys Arg Thr Arg Glu Ala Met Tyr Leu Glu Ala Val Lys
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 Gln Gly Glu Ile Ala Asn Leu Asp Phe Ser Pro Met Val Phe Ile
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 Val Asp Gly Ile Ser Arg Phe Gln Gln Thr Ile Asp Ala Ser Ile
 1385 1390 1395
 Gln Asp Lys Met Ala Met Phe Met Lys Ser Tyr Ala His Leu Gly
 1400 1405 1410
 Phe His Phe Ile Pro Ala Gly Asn His Ser Glu Phe Thr Lys Gly
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 Tyr Asp Ser Leu Thr Ser Glu Val Lys Gln Val Arg His Ala Met
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 1445 1450 1455
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 gaatataatc gaacaaaaca aggacgcaca ggaagggata atccaatgat tctgtatacg 180
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gatgtaaaca gcgtgccact tttagtcgag atgaacggag aggaagcaag ggacgttcag	300
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tccagaggaa aatcgagcc gaaaaaaggc tgcttttctt ttgtttttac attttttaac	480
acgcagtaag gtgatggaac atg gca aaa aga aaa cga aaa tca aca aag aaa	533
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caa aaa caa gga aaa aaa cgg atc cat ctt aaa ttt gaa ttg tac gga	581
Gln Lys Gln Gly Lys Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly	
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Leu Ile Cys Ile Ala Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val	
30 35 40	
gca ggg caa acg ttc att tac atg ttc cgc ttt ttc gcc ggt gaa tgg	677
Ala Gly Gln Thr Phe Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp	
45 50 55	
ttc atc ctt tgc ctt ctc ggc ctc ttt tta acg ggc ttg tct tta ttt	725
Phe Ile Leu Cys Leu Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe	
60 65 70 75	
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Trp Lys Lys Lys Thr Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu	
80 85 90	
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Tyr Cys Ile Ile Ala Ser Met Leu Leu Leu Ser His Val Gln Leu Phe	
95 100 105	
cag cat ttg acc gaa agg gga atg gtt cag tct ccg agc gtg atc caa	869
Gln His Leu Thr Glu Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln	
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Asn Thr Trp Glu Leu Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser	
125 130 135	
cct gat ctt gga ggc gga atg att gga gcc ctt tta ttc gcg gcg tca	965
Pro Asp Leu Gly Gly Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser	
140 145 150 155	
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Tyr Phe Leu Phe Ala Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu	
160 165 170	
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Ile Leu Ile Gly Leu Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr	
175 180 185	
ctg atc aaa tgg atg acc ccg gtc gcc tcc ttc atg aaa aac cag tgg	1109
Leu Ile Lys Trp Met Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp	
190 195 200	
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Gln Ala Phe Leu Ala Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys	
205 210 215	
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Lys Lys Ser Gly Lys Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser	
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gaa gag cct gta caa gaa gcg gac ctt gat cca gat ccg gtt att caa Glu Glu Pro Val Gln Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln 240 245 250	1253
tca gaa ccg att att tca agc ttt tcc gac cgt gat gaa aag ccc gaa Ser Glu Pro Ile Ile Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu 255 260 265	1301
gtt caa gct tac gaa gct ccg gcg gct cct gct gaa cct cct gct gag Val Gln Ala Tyr Glu Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu 270 275 280	1349
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ttt aca gag cta gaa aac aag gat tac cag ctt ccg tcg att caa ttg Phe Thr Glu Leu Glu Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu 300 305 310 315	1445
ctg gat gat ccg aag cac aca ggg cag cag gcg gat aaa aag aat att Leu Asp Asp Pro Lys His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile 320 325 330	1493
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gaa gtc tat cct gat gtg ggc gtc aaa gtc agc aaa att gtc aac tta Glu Val Tyr Pro Asp Val Gly Val Lys Val Ser Lys Ile Val Asn Leu 365 370 375	1637
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gcc ccg atc ccc gga aaa tcg gcg att gga atc gaa gtg ccg aat gcg Ala Pro Ile Pro Gly Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala 400 405 410	1733
gaa gtg gcg atg gtt tcc ttg aaa gaa gtg ctt gaa tcg aaa ctg aat Glu Val Ala Met Val Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn 415 420 425	1781
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gga gaa gcg gta ttg gca gag ctg aac aaa atg ccc cac ctt ctt gtt Gly Glu Ala Val Leu Ala Glu Leu Asn Lys Met Pro His Leu Leu Val 445 450 455	1877
gca gga gcg acc gga agc ggg aaa agc gtc tgt gtc aac ggg atc att Ala Gly Ala Thr Gly Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile 460 465 470 475	1925
aca agc att ttg atg agg gca aag ccc cac gaa gtg aag atg atg atg Thr Ser Ile Leu Met Arg Ala Lys Pro His Glu Val Lys Met Met Met 480 485 490	1973
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aag aaa gtc gtc aac gaa atg gag cgg cgc tac gaa ttg ttt tct cac	2117
Lys Lys Val Val Asn Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His	
525 530 535	
acg gga acg aga aat atc gaa ggg tat aac gac tat att aaa cgg atg	2165
Thr Gly Thr Arg Asn Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met	
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Asn Ala Ala Glu Glu Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val	
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Ile Val Asp Glu Leu Ala Asp Leu Met Met Val Ala Ser Ser Asp Val	
575 580 585	
gaa gac tcg atc aca agg ctt tcg caa atg gcc agg gcg gcg ggc atc	2309
Glu Asp Ser Ile Thr Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile	
590 595 600	
cac ctg atc att gcg acg cag agg cct tcg gtc gat gtt atc aca ggg	2357
His Leu Ile Ile Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly	
605 610 615	
gtc att aaa gcc aac att ccg tca agg atc gct ttc agc gta tcg tct	2405
Val Ile Lys Ala Asn Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser	
620 625 630 635	
cag acc gac tcc agg acg att ctt gat atg gga ggc gct gaa aaa ctt	2453
Gln Thr Asp Ser Arg Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu	
640 645 650	
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Leu Gly Arg Gly Asp Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro	
655 660 665	
ctc cgc gtt caa ggt gcc ttt ctg tca gac gaa gaa gtt gaa aaa gtt	2549
Leu Arg Val Gln Gly Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val	
670 675 680	
gtc gat cac gtc atc agc cag caa aaa gcc caa tac caa gaa gaa atg	2597
Val Asp His Val Ile Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met	
685 690 695	
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Ile Pro Glu Glu Thr Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu	
700 705 710 715	
tat gac gaa gcg gtc gca ctt gtg gtc agc atg cag acg gct tct gta	2693
Tyr Asp Glu Ala Val Ala Leu Val Val Ser Met Gln Thr Ala Ser Val	
720 725 730	
tcc atg ctg caa agg aga ttc cgc atc ggc tat aca aga gcg gcg cgg	2741
Ser Met Leu Gln Arg Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg	
735 740 745	
ctt atc gat gcc atg gaa gag cgg gga atc gtc ggc cca tat gaa gga	2789
Leu Ile Asp Ala Met Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly	
750 755 760	
tca aaa ccc cgt gaa gtt ctc ttg tca aaa gag caa tac gaa gaa ctc	2837
Ser Lys Pro Arg Glu Val Leu Ser Lys Glu Gln Tyr Glu Glu Leu	
765 770 775	

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 Ser Ser
 780

atctatttat ttatttgaca aaacatgata tagttatcct caattaaaga taatttgaat 2953
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 35 40 45

Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp Phe Ile Leu Cys Leu
 50 55 60

Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe Trp Lys Lys Lys Thr
 65 70 75 80

Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu Tyr Cys Ile Ile Ala
 85 90 95

Ser Met Leu Leu Leu Ser His Val Gln Leu Phe Gln His Leu Thr Glu
 100 105 110

Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln Asn Thr Trp Glu Leu
 115 120 125

Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser Pro Asp Leu Gly Gly
 130 135 140

Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser Tyr Phe Leu Phe Ala
 145 150 155 160

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 180 185 190
 Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp Gln Ala Phe Leu Ala
 195 200 205
 Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys Lys Lys Ser Gly Lys
 210 215 220
 Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser Glu Glu Pro Val Gln
 225 230 235 240
 Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln Ser Glu Pro Ile Ile
 245 250 255
 Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu Val Gln Ala Tyr Glu
 260 265 270
 Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu Pro Glu Ile Gly Glu
 275 280 285
 Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr Phe Thr Glu Leu Glu
 290 295 300
 Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu Leu Asp Asp Pro Lys
 305 310 315 320
 His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile Tyr Asp Asn Ala Arg
 325 330 335
 Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val Lys Ala Lys Val Thr
 340 345 350
 Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr Glu Val Tyr Pro Asp
 355 360 365
 Val Gly Val Lys Val Ser Lys Ile Val Asn Leu Ser Asp Asp Leu Ala
 370 375 380
 Leu Ala Leu Ala Ala Lys Asp Ile Arg Ile Glu Ala Pro Ile Pro Gly
 385 390 395 400
 Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala Glu Val Ala Met Val
 405 410 415
 Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn Asp Arg Pro Asp Ala
 420 425 430

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Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser Gly Glu Ala Val Leu
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 465 470 475 480
 Arg Ala Lys Pro His Glu Val Lys Met Met Met Ile Asp Pro Lys Met
 485 490 495
 Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His Leu Leu Ala Pro Val
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 Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu Lys Lys Val Val Asn
 515 520 525
 Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His Thr Gly Thr Arg Asn
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 545 550 555 560
 Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val Ile Val Asp Glu Leu
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 580 585 590
 Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile His Leu Ile Ile Ala
 595 600 605
 Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Val Ile Lys Ala Asn
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 625 630 635 640
 Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp
 645 650 655
 Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro Leu Arg Val Gln Gly
 660 665 670
 Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val Val Asp His Val Ile
 675 680 685
 Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met Ile Pro Glu Glu Thr
 690 695 700

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Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu Tyr Asp Glu Ala Val
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Ala Leu Val Val Ser Met Gln Thr Ala Ser Val Ser Met Leu Gln Arg
725 730 735

Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg Leu Ile Asp Ala Met
740 745 750

Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly Ser Lys Pro Arg Glu
755 760 765

Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu Ser Ser
770 775 780